

OM of: US-09-722-377-1 to: EST:* out_format : pfs
Date: Jul 23, 2002 3:02 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09722377/runat_19072002_111534_29783/app_query.fasta_1.597
-DB=EST -QFMT=fastap -SUFFIX=oli.rst -GAPOP=4.500 -GAPEXT=0.050
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=300 -ALIGN=15
-MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09722377_@CGN1_1_2896 -NCPU=6
-ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY
-WAIT -THREADS=1

Search information block:

Query: US-09-722-377-1
Query length: 533
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1685.370000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:
Sequence Strd Orig ZScore EScore Len ! Documentation ..

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 12:19:36 ; Search time 54.54 Seconds
(without alignments)
7214.978 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaagggt.....tttccttcagccagggatga 1602

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 300

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description

No matches found

Search completed: July 23, 2002, 13:31:29
Job time: 4313 sec

OM of: us-09-722-377-1 to: Issued_Patents_NA:* out_format : pfs
Date: Jul 23, 2002 3:37 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL=framet_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09722377/runat_19072002_111535_29853/app-query.fasta_1.597
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oli.rni -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality
-THR_MIN=300 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09722377@cgnl_1_52 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-722-377-1
Query length: 533
Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
Search time (sec): 50.610000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:	Strd Orig	ZScore	Escore	Len	! Documentation	..
Sequence						

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:27:21 ; Search time 1672.7 Seconds
(without alignments)
12926.479 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcgacaaaaaagggt.....tttcctcagccagggatga 1602

Scoring table: OLIGO_NT
Gapop 60.0 , Gapext 60.0

Searched: 13736207 segs, 6748477542 residues

Word size : 300

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_estlhum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estloy:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	650	40.6	700	10 BE519781	BE519781 HV_CEB002
2	570	35.6	605	9 AV835197	AV835197 AV835197
3	479	29.9	669	9 AV945501	AV945501 AV945501
4	451	28.2	798	10 BE558835	BE558835 HV_CEB002
5	356	22.2	402	9 AV945620	AV945620 AV945620

ALIGNMENTS

RESULT 1
BE519781 700 bp mRNA linear EST 23-OCT-2001
LOCUS HV_CEB0021D05f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEB0021D05f, mRNA sequence.
ACCESSION BE519781

VERSION BE519781.2 GI:13266203
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum.
1 (bases 1 to 700)

AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wel,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library

JOURNAL Unpublished (2001)
COMMENT On Aug 8, 2000 this sequence version replaced gi:9743969.
Contact: Wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

FEATURES
source
Total hg bases = 586
Seq primer: AATTACCCCTCCTAAAGCG
High quality sequence start: 4
High quality sequence stop: 664.
Location/Qualifiers
1..700
/organism="Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEB0021D05f"
/clone_lib="Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP, Site_1: EcoRI; Site_2: XhoI; C.I. 16151 (Mla6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wel, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum , Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

BASE COUNT 149 a 210 c 191 g 150 t
ORIGIN

Query Match 40.6%; Score 650; DB 10; Length 700;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES	LOCATION/Qualifiers
QY 280	gtcatgtgccccctgtcaagcgcgcgcacccgagggcccgcaagccagcaagtaagtcgtgactac 339
Db 1	GTCAATGTGGCCCTGCAGACGGCGGCACCGAGGGGCCGCAAGCCCAAGTAAGTGTGACTAC 60
QY 340	tgcccggaagcgcaaggttgcgcctcatgtctccacgcgcagcttgcaccagctgcacgtcttc 399
Db 61	TGCCCGGAGGGGCAAGGTGGCGCTCATGTCCACGGCGAGCTTGACACCAGCTGCACGTCCTTC 120
QY 400	atcttcgtgtcgcgcgtcttcacatgtcacctacagcgtcatcacatagctctcaagccgt 459
Db 121	ATCTTCGTGCTCGCGGCTTCCATGTCACTACCTACAGCGTTCATCACCATTAGCTCTTAAGCCGT 180
QY 460	ctcaaaatgagaacatggaagaatatgagacagagaccaacttccttgaataaccagttc 519
Db 181	CTCAAAATGAGAACTAGGAAGAAATGGAGACAGAGACCACCTCCTTGAATACCAAGTTC 240
QY 520	gcaaatgatcctgcacgcgttccggtttcacgcacacagacgtctgtcgtgaagcgccacctg 579
Db 241	GCAAAATGATTCCTGCACGCTTCGGGTTCACGCACACAGAGCTGCTCGTGAAGCGCCACCTG 300
QY 580	ggcctctccagcacccctggcatcagatgtgtgtgtgccttctcagcgagttcttcagg 639
Db 301	GGCCTCTCCAGCACCCCTGGCATCAGATGGGTGTGGGCTTCTTCAGGCAGTTCCTTCAGG 360
QY 640	tcagtcaccaaggttgactacacctgaccttgaggcaggttcatcaacgcgcatattgtcg 699
Db 361	TCAGTCACCAAGGTGAGTACTACCTGACCTTGAGGGGCAAGCTTCATCAACGGCATTTGTGG 420
QY 700	caaaacagcaagttcgacttccacaagaatcacatcaagaaggtcgatgtgagagcagcttcaag 759
Db 421	CAAAACAGCAAGTTCGACTTCCACAAAGTACATCAAGAGGTGATGGAGAGCAGCACTTCAAG 480
QY 760	gtcgtcgtcgcgcacagcttcccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 819
Db 481	GTGCTGCTCGGCATCAGCCTCCCGCTGTGGGGGTGTGGCGATCCTCACCCCTTTCCTTGGAC 540
QY 820	atcaatgggtgtgcgcagcgtcatctgtgattcttcatccctctcgtgatcctctgtgtgt 879
Db 541	ATCAATGGGGTGTGGCAGCTCATCTGTGATTCTTTCATCCCTCTCGTATCCTCTTGTGTGT 600
QY 880	gttgaaccaagctgagagatgatcatcatgatgagatggcccttgagatcca 929
Db 601	GTTGAACCAAGCTGAGATGATCATCATGAGATGGCCCTGGAAGATCCA 650
RESULT 2	
AV835197	605 bp mRNA linear EST 22-JUN-2001
LOCUS	AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION	spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah26o13, mRNA sequence.
ACCESSION	AV835197
VERSION	AV835197.1 GI:14527286
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. spontaneum.
ORGANISM	Hordeum vulgare subsp. spontaneum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
	; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 605)
AUTHORS	Sato, K.
TITLE	Barley EST sequencing project in NIG and Okayama Univ
JOURNAL	Unpublished (2001)
COMMENT	Contact: Kazuhiro Sato Research Institute for Bioresources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kazsato@rib.okayama-u.ac.jp, URL: http://www.rib.okayama-u.ac.jp/barley/ Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission: http://www.shigen.nig.ac.jp/barley/Barley.html. database: http://www.shigen.nig.ac.jp/barley/Barley.html.

Source 1. 605
 /organism="Hordeum vulgare subsp. spontaneum"
 /cultivar="H602"
 /db_xref="taxon:77009"
 /clone="bah26013"
 /clone_lib="K. Sato unpublished cDNA library: Hordeum
 vulgare subsp. spontaneum top three leaves adult, heading
 stage"
 /issue_type="top three leaves"
 /dev_stage="adult, heading stage"
 BASE COUNT 131 a 188 c 163 g 122 t 1 others
 ORIGIN

Query Match 35.6%; Score 570; DB 9; Length 605;
 Best Local Similarity 100.0%; Pred. No. 9.4e-276;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	236	accaccatcatgcgaagaatatgcatctccgagatgcgcgcgacgtcatgtgcccctgca	295
Db	36	ACCCCATCATCGCCACAGATATGCATCTCCGAGATGCCGCCGACGTCATGTGCCCTGCA	95
QY	296	agcgcgcacccgagggccgcaagcccagcaagtaagtaagtaactgactgcccggagggcaag	355
Db	96	AGCGCGCACCCGAGGGCCGCAAGCCGACGAGTACGTTGACTACTGCCCGGAGGCAAGG	155
QY	356	tggcgcctcatgtccacggggcagcttgcaccagctgcaacgtctctcatctctgtgcgcgg	415
Db	156	TGGCGCTCATGTCCACGGGCAAGCTTGACACGACGTCGACGCTTTCATCTTCGTGCTGCGG	215
QY	416	tcttccatgtcaccttaacagcgtcatcatcaccatagctctaaagccgtctcaaatgagaaat	475
Db	216	TCTTCCATGTCAACCTACAGCGTCATCAACCATAGCTCTAAGCCGCTCAAAATGAGAACAT	275
QY	476	ggaagaatatggagagacagagaccacctccttggaaataacagttcgcaaatgatctcgac	535
Db	276	GGAAGAATGGAGACAGAGACCACCTCCTTGGAAATACCAGTTCGCAATGATCCTGCAC	335
QY	536	ggttccggttcaagcacaagacgtcgttctgtgaagcgcaacctggyccctctccagcacc	595
Db	336	GGTTCGGTTCACGCGCACGACGTCGTCTGTAAGCGCCACCTGGGCCCTCTCCAGCACCC	395
QY	596	ctggcatcagatggtgtgtgcccctctcaggcagttcttcaggtcagtcaccgaagtgg	655
Db	396	CTGGCATCAGATGGGTGTGGCCTTCTTCAGGCAGTTCTTCAGGTCAAGTCACCAAGGTGG	455
QY	656	actacctgaccttgaggcaggcttcatcaacgcgcatlgtcgcaaaaacagcaagttcg	715
Db	456	ACTACCTGACCTTGAGGGGAGGCTTCATCAACGCGCAATTGTGCGCAAAACAGCAAGTTGG	515
QY	716	acttccacaagtacatcaagaagtcgatgagagacacttcaaggtcgtcgtcgcatca	775
Db	516	ACTTCCACAAGTACATCAAGAGGTGATGAGGACGACTTCAAGGTGCTGTGGCATCA	575
QY	776	gcctcccgctgtgggtgtgtgcgatactca	805
Db	576	GCCCTCCCGCTGTGGGGTGTGGCGATCCTCA	605

RESULT 3
 AV945501/c 669 bp mRNA linear EST 18-JAN-2002
 LOCUS AV945501 K. Sato unpublished cDNA library, strain H602 adult,
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
 CDNA clone bah26013 3', mRNA sequence.
 ACCESSION AV945501
 VERSION AV945501.1 GI:18241298
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. spontaneum.
 ORGANISM Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 669)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source Location/Qualifiers

1. 669
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
131 a 182 c 192 g 163 t 1 others

BASE COUNT 131 a 182 c 192 g 163 t 1 others
ORIGIN

Query Match 29.9%; Score 479; DB 9; Length 669;
Best Local Similarity 99.8%; Pred. No. 6.7e-230;
Matches 529; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1015 ttcttcatacactgacgttgttccagaacgcgttcagatgycgcgaatttgttgaca 1074
|||||
Db 669 TTCTTCATACACCTGACGTGTGTCCAGAACGCGTTTCAGATGGCGCAATTGTGTGACA 610
OY 1075 gtggccaacgcgcgttgaaagaatgctaccacacgcagatcgggtgagcatcatgaag 1134
|||||
Db 609 GTGGCCACGCCCGGCTTGAAGAAATGCTACCACACGACAGATCGGGCTGACATCATGAAG 550
OY 1135 gtgggtgtgggtagctctccagttcctctgcagctatatagaccttcccccttacgcg 1194
|||||
Db 549 GTGGTGTGGGGTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCG 490
OY 1195 ctcgtcacacagatggatcaaacatgaagaggttcattcttcgacgagcagaacgtccaag 1254
|||||
Db 489 CTCGTACACAGATGGATCAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAG 430
OY 1255 gcgctaccaactgycggaacacgcgcaagagaagaagaagtccgagacacgcgacatg 1314
|||||
Db 429 GCGCTCACCAACTGGCGGAACACGGCCAAAGAGAGAAAGTCCGAGACACGGACATG 370
OY 1315 ctgattgctcagatgacgcgacgcaacacgcgagcaggtcgtcgccgatagcgagc 1374
|||||
Db 369 CTGATGGCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTGTCGCGATGCCGAGC 310
OY 1375 cggggtcatcatcaccctgtcacctgtctacaaggggcatggggcggtcggacgacccccag 1434
|||||
Db 309 CGGGGCTCATCAACCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAG 250
OY 1435 agcgcgcccaactcgcgaagagcccaagcagaggtagggacatgtaccggttgtgtg 1494
|||||
Db 249 AGCGCGCCCACTTCGCCAAGGACCCACAGAGAGGCTAGGGACATGTACCCGGTGTGTG 190
OY 1495 gcgcacccggtgcacagactaaatcctaacgacagagaggtccgcctc 1544
|||||
Db 189 GCGCACCCGGTGCACAGACTAAATCCTAACGACAGAGAGGAGGTCCGCCTC 140

RESULT 4
BE558835 798 bp mRNA linear EST 23-OCT-2001
LOCUS BE558835
DEFINITION HV_CEB0020108f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEB0020108f, mRNA sequence.
ACCESSION BE558835

VERSION BE558835.3 GI:16336267
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 798)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.

TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library

JOURNAL Unpublished (2001)
COMMENT On Aug 14, 2000 this sequence version replaced gi:13266126.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu

FEATURES
source Total hg bases = 458
Seq primer: AATTACCCCTCACTAAAGG
High quality sequence stop: 561.
Location/Qualifiers

1. 798
/organism="Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
/clone_lib="HV_CEB0020108f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 153 a 244 c 241 g 158 t 2 others
ORIGIN

Query Match 28.2%; Score 451; DB 10; Length 798;
Best Local Similarity 99.8%; Pred. No. 8.9e-216;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 atgtcgacaaaagggtgctcgcgcgaggagctgcggagagccgctcgtggcggtg 60

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Db 197 ATGTCGACAAAAAGGGTCCCGCGCGGAGAGCTGCCGAGACGCCGCTCGTGGCGGTG 256
QY 61 ggggtgtcttcgcccgaatgtgtctgttccgtccatcgtgaacacggtccacaag 120
Db 257 GCGGTGGTCTTCGCCGCGCATGTGCTCGTGTCCGCTCATGGAGCACGGCTCCACAAG 316
QY 121 ctggccattgttccagcaccgycacaaagaagccctgtgagagcgctggaagatg 180
Db 317 CTGGCCATGTGTTCCAGCACCGGACACAAGAGGCCCTGTGGAGGCCCTGGAGAAGATG 376
QY 181 aagcgagagctcatgtgtgtgtgttccatccctgtctcctcctcgtcagcagagccc 240
Db 377 AAGCGGAGCTCATGCTGTGGGCTTCATATCCCTGCTCTCATCTGTCACGACGACCCC 436
QY 241 atcctgcgaagatatgtcattcccgagagatgcccgcagctcatgtgtccctgcaagcg 300
Db 437 ATCATGCCCAAGATATGATTCGAGGATGCCGCCGACGTCATGTGCGCTGCAAGCGC 496
QY 301 ggcacgagggcgccgaagcccgcaagtaagctgtgactactgcccggagggcaagtggcg 360
Db 497 GGCACCGAGGGCGCCGACGCGCAAGCAAGTACGTGACTACTGCCCGGAGGGCAAGTGGCG 556
QY 361 ctcatgtccacgagcgagcttgcacacagctgcagcttctcctcctcgtgtcgtgtc 420
Db 557 CTGATGTCCACGCGGACGCTGACACCAAGCTGACACGCTTCATCTTCGTCGCGCTCTTC 616
QY 421 catgtcacctacagcgtcatcaccatagctcctaagccgtctcaaatgagaatggaag 480
Db 617 CATGTCACTTACAGCGCTCATACCATAGCTTAAGCCGCTCTCAAAATGAGAACATGGAAG 676
QY 481 aaatgggagagagagaccact 502
Db 677 AAATGGAGACAGAGACCACCT 698
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RESULT 5
AV945620/c 402 bp mRNA linear EST 18-JAN-2002

LOCUS AV945620 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah27g01 3', mRNA sequence.

ACCESSION AV945620
VERSION AV945620
KEYWORDS AV945620.1 GI:18241417
SOURCE EST.

ORGANISM Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 402)
AUTHORS Sato, K., Saisho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
source
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location/Qualifiers
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah27g01"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"

BASE COUNT 60 a 116 c 127 g 96 t 3 others
ORIGIN

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Query Match 22.2%; Score 356; DB 9; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5.4e-168;  
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1189 taacgctcgtcacacagatggatcaaacatgaagagttccatcttcacgagcagag 1248  
Db 361 TACGCGCTGTCACACAGATGGATCAAAACATGAGAGCTTCATCTTCAGAGCAGACG 302  
QY 1249 tccaagcgctcaccaactgycgaacacgycgaaggaagaagaagtcgagacag 1308  
Db 301 TCCAAGCGCTCACCAACTGGCGGAACACGCGCAAGAGAAAGATCCGAGACAG 242  
QY 1309 gacatgtgatgtgtcagatgaltcggcagcgaacacgagcgaagctcgcgagtg 1368  
Db 241 GACATGCTGATGGCTCAGATGATCGCGAGCGCAACCGAGGCTGCTGCGCGATG 182  
QY 1369 ccgagccggggtcatcaccgltgcacctgttcaaaaggagcatggggtcggagac 1428  
Db 181 CCGAGCGGGGCTCATCACCCGTCACCTGCTTCAAGGGCATGGGGCTCGGACGAC 122  
QY 1429 ccccaagcgcgcccaactcgcgaagagcccaaggaaggttaggacatgtaccggt 1488  
Db 121 CCCAGAGCGCGCCACCTCGCCAAAGAGCCCAAGAGGCTAGGACATGTACCCGTT 62  
QY 1489 gtgtgtgcgacccggtgcagagactaatcctaagcagagagaggtccgctc 1544  
Db 61 GTGTGGCGCACCCGGTGCACAGACTAAATCTTAACGACAGGAGGATCGCGCTC 6
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Search completed: July 23, 2002, 12:50:50
Job time: 5009 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:23:25 ; Search time 43.76 Seconds
(without alignments)
1170.375 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALREADIPSADEFSFG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2788	100.0	533	2	T04481	Mlo protein - barl
2	1941	69.6	544	2	T05952	Mlo-hl protein - b
3	1792	64.3	537	2	T03797	probable mlo prote
4	1253.5	45.0	573	2	B86247	hypothetical prote
5	1234.5	44.3	583	2	H96640	hypothetical prote
6	1220.5	43.8	570	2	T02582	H. vulgare Mlo pro
7	1101.5	39.5	501	2	B84748	similar to Mlo pro
8	1088	39.0	574	2	F84552	similar to Mlo pro
9	1061	38.1	580	2	B84552	similar to Mlo pro
10	1049	37.6	443	2	E96495	hypothetical prote
11	932.5	33.4	526	2	T01089	hypothetical prote
12	927	33.2	496	2	T00691	H. vulgare Mlo pro
13	853.5	30.6	429	2	T09888	hypothetical prote
14	790.5	28.4	485	2	T47469	hypothetical prote
15	631	22.6	507	2	H86393	protein T24P13.8 l
16	499.5	17.9	447	2	A86244	Barley Mlo protein
17	114	4.1	628	2	AG1469	transporter homolo
18	105.5	3.8	574	2	D91159	probable transport
19	105.5	3.8	574	2	B86005	probable transport
20	105	3.8	628	2	AF1108	transporter homolo
21	103.5	3.7	770	2	G90506	conserved hypothet
22	102.5	3.7	574	2	E65135	hypothetical 64.6k
23	98.5	3.5	453	2	B95135	MATE efflux family
24	97.5	3.5	596	2	T19740	hypothetical prote
25	97	3.5	401	2	E81436	transmembrane tran
26	95.5	3.4	443	2	F71929	heat shock protein
27	95.5	3.4	506	2	A33416	nuclear factor 1 -
28	95	3.4	335	2	T32209	hypothetical prote
29	95	3.4	453	2	D98003	conserved hypothet

30	95	3.4	3071	2	T50345	vacuolar protein s
31	94.5	3.4	303	2	E88241	protein T22C8.1 (l
32	94.5	3.4	303	2	T25114	hypothetical prote
33	94.5	3.4	338	2	E72264	conserved hypothet
34	94	3.4	395	2	S73732	MG306 homolog A05-
35	94	3.4	599	2	G90476	probable Na+/H+ an
36	93.5	3.4	369	2	I64234	competence locus E
37	93.5	3.4	443	1	D64584	heat shock protein
38	93.5	3.4	554	2	T43211	cytoplasmic signal
39	93.5	3.4	666	2	T43171	hypothetical prote
40	93.5	3.4	672	2	T24507	nitrite extrusion
41	93.5	3.4	951	2	AC3628	probable integral
42	92.5	3.3	167	2	C81358	cytochrome-c oxida
43	92.5	3.3	262	1	OTFF3Y	cytochrome-c oxida
44	92.5	3.3	262	2	T09805	NADH dehydrogenase
45	92.5	3.3	512	2	F71839	

ALIGNMENTS

RESULT	1	Query Match	Best Local Similarity	Score	DB 2;	Length	533;
M04481	Mlo protein - barley	100.0%;	100.0%;	Pred. No. 5.9e-232;	Mismatches	0;	Indels
C;Species: Hordeum vulgare (barley)							
C;Date: 23-Apr-1999	#sequence_revision 23-Apr-1999						
C;Accession: T04481							
R;Panstruga, R.; Buschges, R.; Piffanelli, P.; Schulze-Jefet, P.							
Nucleic Acids Res. 26, 1056-1062, 1998							
A;Title: A contiguous 60kb genomic stretch from barley reveals molecular evidence for							
A;Reference number: Z15372; MUID:98128007							
A;Accession: T04481							
A;Status: preliminary; translated from GB/EMBL/DDBJ							
A;Molecule type: DNA							
A;Residues: 1-533 <PAN>							
A;Cross-references: EMBL:Y14573; NID:g2894376; PIDN:CAA74909.1; PID:g2894377							
A;Experimental source: cv. Ingrid							
C;Genetics:							
A;Gene: MLO							
A;Map position: 4							
A;Introns: 43/3; 116/3; 155/3; 176/1; 204/3; 229/3; 259/2; 276/1; 289/3; 359/3; 402/3							
C;Superfamily: barley pathogen resistance protein Mlo							
QY	1	MSDKKGVPARELPETPSWAAVFAAMVLSVLMHGLHKLGHWFQHRKKALWEALEKM	60				
Db	1	MSDKKGVPARELPETPSWAAVFAAMVLSVLMHGLHKLGHWFQHRKKALWEALEKM	60				
QY	61	KAELMLVGFISLLIVTQDPIAKICISEDADVMMPCKRGTEGRKPSKYVDYCPGKVA	120				
Db	61	KAELMLVGFISLLIVTQDPIAKICISEDADVMMPCKRGTEGRKPSKYVDYCPGKVA	120				
QY	121	LMSTGSLHQLHVEIFVLAVFHVTVSVITIALSRLKMTWKKTETTSLEYQFANDPARF	180				
Db	121	LMSTGSLHQLHVEIFVLAVFHVTVSVITIALSRLKMTWKKTETTSLEYQFANDPARF	180				
QY	181	RFTHQTSFYKRLHGLSTPGIRWVVAFFRQFFRSVTQVDYTLRAGFINAHLSONSKFDF	240				
Db	181	RFTHQTSFYKRLHGLSTPGIRWVVAFFRQFFRSVTQVDYTLRAGFINAHLSONSKFDF	240				
QY	241	HKYIKRSMEDDFKVVVIGISLPLMGVAITLFLDINGVGTLLIWSIFPLVILLCVGTKLEM	300				
Db	241	HKYIKRSMEDDFKVVVIGISLPLMGVAITLFLDINGVGTLLIWSIFPLVILLCVGTKLEM	300				
QY	301	TIMEALEIQDRAVYIKGAPVVEPSNKFVHRPDVLFIFHLTFQNAFQMAHFVWTV	360				
Db	301	TIMEALEIQDRAVYIKGAPVVEPSNKFVHRPDVLFIFHLTFQNAFQMAHFVWTV	360				
QY	361	TPGLKKCYHTQIGLSIMKVVVGLALQFLCSTWTFPPLVALVTQMGSNMKSIFDEQTSKAL	420				

|||||
Db 361 TPGLKKCYHTQIGLSIMKVVYGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
QY 421 TNWRNTAKEKKKVRDQDMLMAQMGIDATPSRGSSPMPSSPVHLLHKGMGRSDDPQSA 480
Db 421 TNWRNTAKEKKKVRDQDMLMAQMGIDATPSRGSSPMPSSPVHLLHKGMGRSDDPQSA 480
QY 481 PTPSPRTQOEARDMPVNVVAHPVHRLNPNDRRRSASSSALADIPSADEFSSQSG 533
Db 481 PTPSPRTQOEARDMPVNVVAHPVHRLNPNDRRRSASSSALADIPSADEFSSQSG 533

RESULT 2
T05952
Mlo-hl protein - barley
C:Species: Hordeum vulgare (barley)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05952
R:Panstruga, R.
submitted to the EMBL Data Library, May 1997
A:Reference number: Z15093
A:Accession: T05952
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-544 <PAN>
A:Cross-references: EMBL:Z95496; PIDN:CAB08860.1
A:Experimental source: cv. Igri
C:Genetics:
A:Gene: Mlo-h1
A:Map position: 4H
A:Introns: 41/3; 139/3; 178/3; 199/1; 282/2; 299/1; 312/3; 382/3
C:Superfamily: barley pathogen resistance protein Mlo

Query Match 69.6%; Score 1941; DB 2; Length 544;
Best Local Similarity 69.5%; Pred. No. 5.3e-159;
Matches 381; Conservative 51; Mismatches 76; Indels 40; Gaps 6;

QY 10 RELPETPSWAVAVFAAMVLSVLMHGLHKGWFGHRRKKALWEALEKKAELMLVGF 69
Db 8 RELSDPTWAVAVCAVMILVSVAMEHALHKGWFGHRRKKALGEALEKKAELMLVGF 67
QY 70 ISLLIVTQDPIAKICISEDADVMWPK-----KGTEGRKPSKY----- 110
Db 68 ISLLIVTQDP-VSRICISKEAGEKMLPKPYDGAGGCKGKDNHRLMLWGSETHRRF 126
QY 111 -----VDYC-PEGKVALMSTGSLHQLHVFIFVLAHFVHTYTSVITIALSRKMKRTWKKE 163
Db 127 LAAPAGVDVCAKQKVALMSAGSMHQLHIFIFVLAHFVHTYTSVITIALSRKMKRTWKKE 186
QY 164 TETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVAAFRRQFFRSVTKVDYLT 223
Db 187 SETASLEYQFANDPSRCRFTHTQTLVRRHLGLSSTPGIRWVAAFRRQFFTSVTKVDYLT 246
QY 224 RAGFINAHLSONSKFDEHKYIKRSMEDDFKVVVGISLPLMGVAILLFLDINGVGLIWI 283
Db 247 RQGFINAHLSONSKFDEHKYIKRSMEDDFKVVVGISLPLMGVAILLFLDINGVGLIWI 306
QY 284 SFIFLVILLCVGTKLEMIEMALEIQDRASVIKGAIFYVPSNKFWEHRPDWVLEFIHL 343
Db 307 SVVPLVILLWGTKLEMIEMALEIHDRSVVKGAPAVEPSNKFWEHRPDWVLEFIHL 366
QY 344 TLFQNAFQMAHFVMTVATPGLKKCYHTQIGLSIMKVVYGLALQFLCSYMTFPLYALVTQM 403
Db 367 TLFQNAFQMAHFVMTVATPGLKKCYHEKMAISIAKVVLGVAQIILCSYITFPLYALVTQM 426
QY 404 GSNMKRSIFDEQTSKALTNRNNTAKEKKKVRDQDMLMAQMGIDATPSRGSSPMPSSRGSSP 463
Db 427 GSNMKRSIFDEQTSKALTNRNNTAKEKKKVRDQDMLMAQMGIDATPSRGSSPMPSSRGSSP 478
QY 464 VHLHKMGSRSDDPQSAPTSPRTQOEARDMPVNVVAHPVHRLNPNDRRRSASSSALADIP 523
Db 479 VHLHKMGSRSDDPQSAPTSPRTQOEARDMPVNVVAHPVHRLNPNDRRRSASSSALADIP 533

QY 524 PSADFSFS 531
Db 534 PGADFGFS 541

RESULT 3
T03797
probable mlo protein - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T03797
R:Panstruga, R.
submitted to the EMBL Data Library, May 1997
A:Reference number: Z15093
A:Accession: T03797
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-537 <PAN>
A:Cross-references: EMBL:Z95353; PIDN:CAB08606.1
A:Experimental source: isolate IR-BB21
C:Genetics:
A:Gene: Mlo-h1
A:Introns: 42/3; 124/3; 163/3; 184/1; 213/3; 238/3; 268/2; 285/1; 298/3; 356/3; 368/3
C:Superfamily: barley pathogen resistance protein Mlo

Query Match 64.3%; Score 1792; DB 2; Length 537;
Best Local Similarity 67.2%; Pred. No. 3.5e-146;
Matches 366; Conservative 54; Mismatches 85; Indels 40; Gaps 12;

QY 9 ARELPETPSWAVAVFAAMVLSVLMHGLHKGWFGHRRKKALWEAL----EKKAEL 64
Db 8 SRELPEPTWAVAVCAVLVLSAMEHGLHNLSH-----KTTAEVLIFLVLSALAE 60
QY 65 MLVGFISLLIVTQDPIAKICISEDADVMWPKRGTE-----GRKPSKYV--DY 113
Db 61 MLGFIISLLIVTQAQAP-ISKICIPKSAANILLPKAGQDAIEEAAASGRSLAGAGGDY 119
QY 114 CP--EGKVALMSTGSLHQLHVFIFVLAHFVHTYTSVITIALSRKMKRTWKMETETSLEY 171
Db 120 CSKFDGKVALMSAKSMHQLHIFIFVLAHFVHTYTCITTMGLGRKMKMKWKWESQINSLEY 179
QY 172 QFANDPARFRFTHQTSFVKRHLG-LSSTPGIRWVAAFRRQFFRSVTKVDYTLRAGFINA 230
Db 180 QFAIDPSRFRFTHQTSFVKRHLGSSSTPGIRWVAAFRRQFFGSVTKVDYTLTMROGFINA 239
QY 231 HLSONSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAILLFLDINGVGLIWIISFIPLVI 290
Db 240 HLSONSKFDFHKYIKRSMEDDFKVVVGISLPLMGVILVLFLDINGVGLIWIISFVPLII 299
QY 291 LLCVGTKLEMIEMALEIQDRASVIKGAIFYVPSNKFWEHRPDWVLEFIHLTLFQNAF 350
Db 300 VLLVGTKLEMIEMALEIQDRATVIGAPAVEPSNKFWEHRPDWVLEFIHLTLFQNAF 359
QY 351 QMAHFVMTVATPGLKKCYHTQIGLSIMKVVYGLALQFLCSYMTFPLYALVTQMGSNMKRS 410
Db 360 QMAHFVMTMATPGLKCFHENIWLISIVEIVIGISLQVLCSYITFPLYALVTQMGSNMKKT 419
QY 411 IFDEQTSKALTNRNNTAKEKKKVRDQDMLMAQMGIDATPSRGSSPMPSSPVHLLHKG 470
Db 420 IFDEQTKALMNMWRKKAMEKKKVRDADAFLAQMSYDF-----ATPASSRSASPVHLLQDH 474
QY 471 MGRSDDPQSAPT--SPRTQOEARDMPVNVVAHPVHRL--NPNDRRRSASSSALADIPSA 526
Db 475 RARSDDPPSPITVASPAPEE--DMYVPAAASRLDLDDPPDRRMMASSS--ADLADS 529
QY 527 DFSES 531
Db 530 DFSES 534
RESULT 4

H. vulgare M10 protein homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 15-Jun-2001
C:Accession: T02582; D84814
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A:Reference number: 214679
A:Accession: T02582
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-570 <R0D>
A:Cross-references: EMBL:AC004697; NID:g3402671; PID:g3402694
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84814
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-570 <STO>
A:Cross-references: GB:AE002093; NID:g3402694; PIDN:AAC28997.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g39200; T16B24.16
A:Map position: 2
A:Introns: 39/3; 59/1; 140/3; 179/3; 200/1; 229/3; 248/3; 280/2; 297/1; 310/3; 368/3; 38
C:Superfamily: barley pathogen resistance protein M10

Query Match 43.8%; Score 1220.5; DB 2; Length 570;
Best Local Similarity 45.3%; Pred. No. 6.2e-97;
Matches 254; Conservative 93; Mismatches 153; Indels 61; Gaps 12;
QY 7 VPARELPETPSMAVAVFAAMVLVSVMELHGLHGHWFQHRHKKALMEALEKKAELM 66
DB 3 IKERSLEETPTMAVAVCVFLVLSIMIEFLHFGHWFKKHKKALSEALEKKAELM 62
QY 67 VGFISLLIVODPIIAKICISEDADVMPCKRGT-----GRK----- 106
DB 63 LGFISLLVLTOTP-VSEICIPRNIAATMPCSNHCEIAKYKDYIDDGRKILEDPSND 121
QY 107 -----PSKYDYDCE-GKVALMSTGLHQLHVFIFVLAVFHVTVSVITIALSRKMR 157
DB 122 FYSRRNLATKGYDKCAEKGVALSAGYIQLHIFVLAVFHVTVSVITIALSRKMR 181
QY 158 TWKKWETETTSLEYOFANDPARFRTHQTSFVKRHLGL-SSTPGIRWVAFFRQFRSVT 216
DB 162 KWKSWERETKTIETQYANDPERFARDTSFGRHNLNWSKSTFLWT-----FFGSVT 235
QY 217 KVDYLTLRAGFINAHLSQNS--KDFHKKYIKRSMEDDFKVVVGISLPLMGVAITLFLDI 274
DB 236 KVDYLTLRHGFIMAHLPAGSAARFDFQYIKERSLEQDFTVVVGISPLWCIAVLFLTNT 295
QY 275 NGVGLTIWISFIPVILLVCGTKLEMIIMEMALEIODRASVIGAPVVEPSNKFVWHRP 334
DB 296 HGWDXYLMLPFLPLVILLVIGAKLQMIISKGLRIQEKGDVVRKGAPEVPGDDLFWFGRP 355
QY 335 DWVLEFIHLTLFQNAFQMAHFVTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTF 394
DB 356 RFLFLHLVLTNAFQLAFFVWSTYEFILKCNFHHKTEDIAIRITMGVLLIOVLSYITL 415
QY 395 PLVALVTQMGSMKRSIFDEQTSKALTNRNTAKKKKVRDMDLMAQMGIDATPSRGSS 454
DB 416 PLVALVTQMGSMRPIIFNDRVANALKKWHAKKQTKHGS-----GSNTPHSSRP 467
QY 455 PMPSRGSSPVHLHKGMRSDDPQ-----SAPTSPTQOEARMYPVVVAHPVHRLNPNDR 510
DB 468 TPTTHGMSPVHLHNTNRNSLDOQTSFTASPSPPRFSYSGQGH-----GHQ-HFFDPESQ 522
QY 511 RRSASSSALADIPSADFSFS 531

Db 523 NHS-----YQREITDSEFSNS 538
RESULT 7
B84748
similar to M10 proteins from H. vulgare [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: B84748
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84748
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: GB:AE002093; NID:g6598814; PIDN:AAC69142.2; GSPDB:GN00139
C:Genetics:
A:Gene: At2g33670
A:Map position: 2
C:Superfamily: barley pathogen resistance protein M10

Query Match 39.5%; Score 1101.5; DB 2; Length 501;
Best Local Similarity 44.2%; Pred. No. 9.3e-87;
Matches 229; Conservative 88; Mismatches 140; Indels 61; Gaps 10;
QY 6 GVPARELPETPSMAVAVFAAMVLVSVMELHGLHGHWFQHRHKKALMEALEKKAELM 65
DB 11 GEPRELDDQTPMAVAVCVFLVLSIMIEFLHFGHWFKKHKKALSEALEKKAELM 70
QY 66 LVGFISLLIVODPIIAKICISEDADVMPCKRGT-----KRGTGRKP--SKYVD----- 112
DB 71 VLGFISLLTTFQGN-YIASICVASRYGHANSFCGPDGSGESKKPKTTEHLERRVLADA 129
QY 113 ---YCEGKVALMSTGLHQLHVFIFVLAVFHVTVSVITIALSRKMRTWKWTETTS 169
DB 130 APAQCKKGYVPLSLNALHGVHIFIFLAVFHVTVSVITIALSRKMRGWKEEVIN- 188
QY 170 EYQFANDPARFRTHQTSFVKRHLGLSSTPGIR-----WVVAFFRQFRSVTKVDYLT 224
DB 189 DHEMNDPSRFRFLHETSFVREHV-----NPMAKNRFSFYWCMCFRQMLRSVRKSDYLTMR 244
QY 225 AGFINAHLSSQNSKDFHKKYIKRSMEDDFKVVVGISLPLMGVAITLFLDINGVGLTIWIS 284
DB 245 HGFISVHLAPGMKFNQYIKRSLDEDFKVVVGISPLMAFVMLFLFDVHGWTAVIT 304
QY 285 FIPVILLVCGTKLEMIIMEMALEIODRASVIGAPVVEPSNKFVWHRPDLVFFIHLT 344
DB 305 MIRPLTLAIGTKLAIIISDMALEIOERNAVIOGMPLVNVSDRHFWSRPAVLHIIHFI 364
QY 345 LFQNAFQMAHFVTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTQMG 404
DB 365 LFQNAFEITYFEFWIWEFGLRSCFHHHRAIIIRVALGVGVQFLCSYITLPLVALVTQMG 424
QY 405 SNMKRSIFDEQTSKALTNRNTAKKKKVRDMDLMAQMGIDATPSRGSSPMPS----- 458
DB 425 STMKRSVFDDQTSKALKNWHKNAKKSE-----TFQQTQPLPLNRPKTG 469
QY 459 ---RGSSPVHLHKGMRSDDPQASAPTSPRQOEARM 493
DB 470 GDIESASPANI-----TASVDVKESDQSQRDL 497
RESULT 8
F84552
similar to M10 proteins from H. vulgare [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001


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C:Accession: F84552
R:lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
neuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: F84552
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <STO>
A:Cross-references: GB:AE002093; NID:g4914369; PIDN:AAD32905.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g17480
A:Map position: 2
C:Superfamily: barley pathogen resistance protein Mlo

Query Match          39.0%; Score 1088; DB 2; Length 574;
Best Local Similarity 42.6%; Pred. No. 1.6e-85;
Matches 245; Conservative 86; Mismatches 152; Indels 92; Gaps 14;

QY 3 DKKGPARELPETPSMAVAVFEAMVLVSLMEHGLKLGHWFOHRKKALWELEKKA 62
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   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1

QY 63 ELMVLGFIISLLIVTQDPIIAKICISEDADAVMPC-----KRTEGRK----- 106
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
Db 92 ELMVLGFIISLLITFGQYIL-DICIPSHVARTMLPCPAPNLKKEDDDNGESHRLLSFEH 150
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1

QY 107 -----PSKYVDYC-PEGKVALMSTGSLHQLHVFIFVLAVPHVTVSITIALSRLKM 156
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Db 151 RFLSGGEASPTK---CTKEGYVELISAEALHQLHLIFFLAIFHVLVSFLTMIGRLKI 206
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1

QY 157 RTWKKWETETTSLEYQFANDPARFRFTHOTSEVKRHLGL-SSTPGIRWVAFFRQFFRSV 215
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
Db 207 RGMKHWENETSSHNTEFTDTSRFLTHETSEVRAHTEFWTRIPFEFFYVGCFFRQFFRSV 266
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1

QY 216 TKVDYLLRAGFINAHLSONSKFDEHKYIKRSMEDDFKVVVGISLPLMGVAILLFLDIN 275
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QY 276 GVGTLWISFIPLVILACVGTKEIMEMALEIODRASVTKGAPVVEPSNKEFWFHRD 335
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QY 336 WVLFEIHLTLFQNAFQMAHFWVTATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFP 395
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
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QY 396 LYALVTQMGSNMKRSIFDEQTSKALTNRNTAKEKKKVRDPTDMLMAQMGIDATPSRGSSP 455
   1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1
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RESULT 9
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similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: B84552
R:lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
neuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: B84552
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-580 <STO>
A;Cross-references: GB:AEO02093; NID:g6598336; PIDN:AAB86520.2; GSPDB:GN00139
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Matches 220; Conservative 75; Mismatches 130; Indels 56; Gaps 8;

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      ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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QY    199 PGIHWVAFFERQFRSVTKVDYLTLRAGFINAHLSQSKFDFHKYIKRSMEDFKVVVGI 258
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C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: E96495
R;Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidops.
A;Reference number: A86141; MUID:21016719
A;Accession: E96495
A;Status: preliminary
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About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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DEFINITION Sequence 2 from Patent WO9804586.

ACCESSION A92828

VERSION A92828.1 GI:6741365

KEYWORDS

SOURCE

ORGANISM barley.
Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

1 (bases 1 to 1602)

REFERENCE Panstruga, R. and Bueschges, R.

POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN

PLANTS

JOURNAL Patent: WO 9804586-A 2 05-FEB-1998;

INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)

FEATURES

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DEFINITION Sequence 7 from Patent WO9804586.
ACCESSION A92833
VERSION A92833.1 GI:6741370
KEYWORDS
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1917)

AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
JOURNAL Patent: WO 9804586-A 7.05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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184 iSglnThrSerPheValLysArgHisLeuGlyLeuSerSerThrProGly 200
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217 sValaspyrleuThrleuArgAlaGlyPheIleAsnAlaHisLeuSerG 234
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LOCUS HVMO 1917 bp mRNA linear PLN 07-MAR-1997
DEFINITION H.vulgare mRNA for M10 protein.
ACCESSION Z83834
VERSION Z83834.1 GI:1877220
KEYWORDS M10 gene.
SOURCE barley.
ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1. (bases 1 to 1917)
Buenschges, R., Hollricher, K., Panstruga, R., Simons, G., Wolter, M.,
Frijters, A., van Daelen, R., van de Lee, T., Diergaarde, P.,
Groenendijk, J., Toepesch, S., Vos, P., Salamini, F. and
Schulze-Lefert, P.
The barley M10 gene: a novel control element of plant pathogen
resistance
Cell 88 (5), 695-705 (1997)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL

2 (bases 1 to 1917)
Panstruga, R.
Direct Submission
Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK

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ORIGIN

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US-09-722-377-1 x HVMLO ..

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Date: Jul 23, 2002 3:41 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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AC	AAV35022;
XX	
DT	13-OCT-1998 (first entry)
XX	
DE	Hordeum vulgare cv. Ingrid MLO gene.
XX	
KW	Barley; MLO; mildew; pathogen; resistance; ss.
XX	
OS	Hordeum vulgare.
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FH	Key
FT	CDS
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FT	1..1602
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XX	WO9804586-A2.
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PD	05-FEB-1998.
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PF	29-JUL-1997; 97WO-GB02046.
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PR	07-MAR-1997; 97GB-0004789.
XX	
PR	29-JUL-1996; 96GB-0015879.
XX	
PR	30-OCT-1996; 96GB-0022626.
XX	
PA	(INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX	
PI	Bueschges R, Panstruga R, Schulzelefert PMJ;
XX	
DR	WPI; 1998-159149/14.

DR P-PSDB; AAW59442.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Claim 2; Fig 2; 150pp; English.

XX The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of Mlo function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.

XX Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;

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ID AAV35026 standard; cDNA; 1917 BP.

AC AAV35026;

DT 13-OCT-1998 (first entry)

XX

DE

Hordeum vulgare MLO gene.

XX

KW Barley; MLO; mildew; pathogen; resistance; ss.

XX

OS Hordeum vulgare.

XX

FH

key Location/Qualifiers

FT CDS

FT polyA_signal

FT /tag= b

XX

PN W09804586-A2.

XX

PD 05-FEB-1998.

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PF 29-JUL-1997; 97WO-GB02046.

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PR 07-MAR-1997; 97GB-0004789.

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PR 30-OCT-1996; 96GB-0022626.

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PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.

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PI Bueschges R, Panstruga R, Schulzelefert PMJ;

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DR WPI: 1998-159149/14.

XX

DR P-PSDB; AAW59443.

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PT

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XX

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Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

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225 ATGTGGACAAAAAGGGGTGCCGGGGAGCTGCCGGAGACCCGCTC 274
17 rTrpAlaValAlaValValPheAlaAlaMetValLeuValSerValLeu 34
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275 GTGGGGGTGGCGGTGCTTCGCCGCCATGGTGCTGTCGTCCTCA 324
34 etGluHisGlyLeuHisLysLeuGlyHisTrpPheGlnHisArgHisLys 50
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325 TGAACACGGCCCTCCACAGCTGGCCATGGTTCACAGCACCGGCACAAg 374
51 LysAlaLeuTrpGluAlaLeuGluLysMetLysAlaGluLeuMetLeuVa 67
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375 AAGGCCCTGTGGAGGGCGCTGAGAGATGAAGCGGAGCTCATGTGCT 424
67 lGlyPheIleSerLeuLeuLeuIleValThrGlnAspProIleIleAla 84
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84 yslIecysIleSerGluAspAlaAlaAspValMetTrpProCysLysArg 100
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475 AGATATGCATCTCCGAGGATGCCGCCGACGTATGTGGCCCTGCAAGCC 524
101 GlyThrGluGlyArgLysProSerLysTyrValAspTyrCysProGluG 117
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117 yLysValAlaLeuMetSerThrGlySerLeuHisGlnLeuHisValPhe 134
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575 CAAGGTGGCGCTCATGTCCACGGGGCAGCTTGCAACAGCTGCACGTC 624
134 lPheValIleuAlaValPheHisValThrTyrSerValIleThrIleAla 150
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|||||
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184 lsglnThrSerPheValLysArgHisIleuGlyLeuSerSerThrProGly 200
|||||
775 ACCAGACGTCGTCGTGGAAGCGCCACCTGGGCTCTCCAGCACCCCTGGC 824
201 lIeArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrly 217
|||||
825 ATCAGATGGGTGGTGGCTTCTTCAGGCACTTCTTCAGGTCAGTCAACAA 874
217 sValAspTyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSer 234
|||||
875 GGTGACTACTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCCG 924
234 lAsnSerLysPheAspPheHisLysTyrIleLysArgSerMetGluAsp 250
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251 AspPheLysValValValGlyIleSerLeuProLeuTrpGlyValAlaI 267
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975 GACTTCAAGGTGCTGTCGGCATCAGCCCTCCGCTGTGGGTGTGGCGAT 1024
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1675 CAAGGACCCAGCAGGAGGTAGGACATGTACCCTGTGTGGTGGCGCAC 1724
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RESULT 2

AAV35026
ID AAV35026 standard; cDNA; 1917 BP.

XX AAV35026;

AC AAV35026; (first entry)

DT 13-OCT-1998

DE Hordeum vulgare MLO gene.
KW Barley; MLO; mildew; pathogen; resistance; ss.

OS Hordeum vulgare.

XX Location/Qualifiers

FH Key 225..1826

FT CDS /tag= a /product= MLO protein 1890..1895

FT polyA_signal /tag= b

XX WO9804586-A2.

XX 05-FEB-1998.

PF 29-JUL-1997; 97WO-GB02046.

XX 07-MAR-1997; 97GB-0004789.

PR 29-JUL-1996; 96GB-0015879.

PR 30-OCT-1996; 96GB-0022626.

XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.

XX Bueschges R, Panstruga R, Schulzelefert PMJ;

XX WPI; 1998-159149/14.

DR P-PSDB; AAW59443.

XX New isolated Mlo gene of barley - used to develop products for the

PT production of transgenic plants which have increased pathogen

PT resistance

XX Disclosure; Fig 7; 150bp; English.

XX The sequence is that of the MLO gene, wild-type Mlo exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of Mlo function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.

SQ Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

Query Match	96.8%;	Score 1551;	DB 19;	Length 1917;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1601; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

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Db	1245	atacacctgacgtctgttccagaacgcgtttcaagatggcgcatlittgtgtgacagltggcc	1304
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QY	1441	ccccactcgcgcaaggaacccagcaggggctagggacatgtaccocggtgtgtgtggcgcac	1500
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QY	1501	ccggtgcacagactaaatcctaacgcagacagggaggtccgcctcgtctgcgcctcgaa	1560
Db	1725	ccggtgcacagactaaatcctaacgcagacagggaggtccgcctcgtctgcgcctcgaa	1784
QY	1561	gccgacatccccagttgcagatltttccttcagccagggatga 1602	
Db	1785	gccgacatccccagttgcagatltttccttcagccagggatga 1826	

RESULT 3

AAV35025

ID	AAV35025	standard; DNA; 2425 BP.
XX		
AC	AAV35025;	

AAV35025; AC

XX
DT 13-OCT-1998 (first entry)

XX
DE Hordeum vulgare MLO gene homologue.

xx Barley; MLO; mildew; pathogen; resistance; ss.
KW

xx
os *Hordeum vulgare.*

XX
PN W09804586-A2.

XX 05-FEB-1998.
PD

XX 29-JUL-1997; 97WO-GB02046.
PF

XX 07-MAR-1997; 97GB-0004789.
PR

PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.

XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.

xx	
PI	Bueschges R, Panstruga R, Schulzelefer

XX
DR WPI; 1998-159149/14.

xx

PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance

XX Disclosure; Fig 6; 150pp; English.

CC The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.

XX
SQ Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;

Query Match 24.9%; Score 399; DB 19; Length 2425;

Best Local Similarity 100.0%; Pred. No. 3.6e-184;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 cagatgggatacaacatgaagaggtccatcttcgacgagcagacgtcccaagcgctcacc 1263
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Db 2011 cagatgggatacaacatgaagaggtccatcttcgacgagcagacgtcccaagcgctcacc 2070

QY 1264 aactggcggacaacggccaaggaagaagaagtcgcgagacacagacatgtatggct 1323
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Db 2071 aactggcggacaacggccaaggaagaagaagtcgcgagacacagacatgtatggct 2130

QY 1324 cagatgatcgcgacgcgacacacgcgagcgcgagctcgtccgacatgcccagcgggctca 1383
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Db 2131 cagatgatcgcgacgcgacacacgcgagcgcgagctcgtccgacatgcccagcgggctca 2190

QY 1384 tcaaccgtgcacctgtctcaacaaggcattggggcggtcggagacgacccccagagcgcgccc 1443
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QY 1504 gtgcacagactaatcctaagcaggaagggtccgcctcgtcgtcgccctcgaagcc 1563
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QY 1564 gacatcccagtgcaatttttccttcagccagggatga 1602
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Db 2371 gacatcccagtgcaatttttccttcagccagggatga 2409

Search completed: July 23, 2002, 13:30:22
Job time: 6946 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:31:46 ; Search time 2110.63 Seconds
(without alignments)
15883.557 Million cell updates/sec

Title: US-09-722-377-2

Perfect score: 1602
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 300

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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32: em_htg_other:*
33: em_htgo_inv:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					

1	1602	100.0	1602	6	A92828	A92828 Sequence 2
2	1602	100.0	1917	6	A92833	A92833 Sequence 7
3	1602	100.0	1917	8	HVMLO	Z83834 H.vulgare m
4	411	25.7	513	8	AF267999	AF267999 Triticum
5	399	24.9	2431	6	A92831	A92831 Sequence 5
6	399	24.9	59748	8	HVCH4H	Y14573 Hordeum vul

ALIGNMENTS

RESULT	1					
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LOCUS	A92828	Sequence 2 from Patent WO9804586.				
DEFINITION	A92828					
ACCESSION	A92828					
VERSION	A92828.1	GI:6741365				
KEYWORDS						
SOURCE						
ORGANISM						

barley.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Hordeum.
1 (bases 1 to 1602)
Panstruga, R. and Bueschges, R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
Patent: WO 9804586-A 2 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
JOURNAL
location/Qualifiers
1. 1602
/organism="Hordeum vulgare"
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/clone="MLO"

BASE COUNT 336 a 488 c 466 g 312 t
ORIGIN

Query Match	100.0%;	Score 1602;	DB 6;	Length 1602;	
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DB	121	CTCGGCCATTGTTCCAGCACCGGCACAAGAGCCCTGTGGAGCGCTGGAGAAGATG	180		
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RESULT 2
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LOCUS A92833 1917 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 7 from Patent WO9804586.
ACCESSION A92833
VERSION A92833.1 GI:6741370
KEYWORDS
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1917)
AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN PLANTS
JOURNAL Patent: WO 9804586-A 7 05-FEB-1998;
FEATURES INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
source Location/Qualifiers
1. 1917
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/clone="MLO"
BASE COUNT 395 a 576 c 553 g 393 t
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3

HYMLO LOCUS 1917 bp mRNA linear PLN 07-MAR-1997
DEFINITION H.vulgare mRNA for Mlo protein.
ACCESSION Z83834
VERSION Z83834.1 GI:1877220
KEYWORDS Mlo gene.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1917)
Buensches, R., Hollricher, K., Panstruga, R., Simons, G., Wolter, M.,
Frijters, A., van Daelen, R., van de Lee, T., Diergaarde, P.,
Groenendijk, J., Toepesch, S., Vos, P., Salamini, F. and
Schulze-Lefert, P.
The barley Mlo gene: a novel control element of plant pathogen
resistance
Cell 88 (5), 695-705 (1997)
JOURNAL 97207016
MEDLINE 2 (bases 1 to 1917)
REFERENCE Panstruga, R.
AUTHORS Direct Submission
JOURNAL Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
FEATURES location/Qualifiers
source 1. 1917
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/db_xref="taxon:4513"
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1827. 1917
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BASE COUNT 395 a 576 c 553 g 393 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D	465	ATCATCGCCACAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC	524
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DEFINITION	Triticum aestivum Mlo-1like protein mRNA, partial cds.		linear
ACCESSION	AF267999		PLN 02-JUN-2001
VERSION	AF267999.1	GI:14279360	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			

OY 388 ctgcacgtctcatcttcgtgctcgcggtcttccatgtcacctacagcgatcaccata 447
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RESULT 5
A92831 A92831 2431 bp DNA linear PAT 22-JAN-2000
LOCUS A92831 Sequence 5 from Patent WO9804586.
DEFINITION A92831
ACCESSION A92831
VERSION A92831.1 GI:6741368
KEYWORDS
SOURCE
ORGANISM
barley.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
AUTHORS 1 (bases 1 to 2431)
TITLE Panstruga,R. and Bueschges,R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
JOURNAL Patent: WO 9804586-A 5 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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DEFINITION Y14573
ACCESSION Y14573
VERSION Y14573.1 GI:2894376
KEYWORDS MLO gene; oligosaccharyltransferase; ribophorin I; RING finger protein.
SOURCE
ORGANISM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
AUTHORS 1 (bases 1 to 59748)
TITLE Panstruga,R., Buschges,R., Piffanelli,P. and Schulze-Lefert,P.
A contiguous 60 kb genomic stretch from barley reveals molecular
evidence for gene islands in a monocot genome
Nucleic Acids Res. 26 (4), 1056-1062 (1998)
JOURNAL 98128007
MEDLINE 2 (bases 1 to 59748)
REFERENCE
AUTHORS Panstruga,R.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1997) R. Panstruga, Sainsbury Laboratory, John
Innes Centre, Colney Norwich NR4 7UH, UK
COMMENT Related entry: Z83834.
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Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: July 23, 2002, 13:27:16
Job time: 6930 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 09:00:27 ; Search time 2116.75 Seconds
(without alignments)
15837.634 Million cell updates/sec

Title: US-09-722-377-2
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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12: gb_sy:*
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14: gb_vi:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DEFINITION	A92828				
ACCESSION	A92828				
VERSION	A92828.1	GI:6741365			
KEYWORDS					
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	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Poideae; Triticeae; Hordeum.				
REFERENCE	1 (bases 1 to 1602)				
AUTHORS	Panstruga,R. and Bueschges,R.				
TITLE	POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN				
JOURNAL	PLANTS				
	Patent: WO 9804586-A 2 05-FEB-1998;				
	INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)				
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ACCESSION Z83834				
VERSION Z83834.1 GI:1877220				
KEYWORDS Mlo gene.				
SOURCE barley.				
ORGANISM Hordeum vulgare				
REFERENCE				
AUTHORS Bueschges,R., Hollricher,K., Panstruga,R., Simons,G., Wolter,M., Frijters,A., van Daelen,R., van de Lee,T., Diergaarde,P., Groenendijk,J., Toepesch,S., Vos,P., Salamini,F. and Schulze-Lefert,P.				
TITLE The barley Mlo gene: a novel control element of plant pathogen resistance				
JOURNAL Cell 88 (5), 695-705 (1997)				
MEDLINE 97207016				
REFERENCE 2 (bases 1 to 1917)				
AUTHORS Panstruga,R.				
TITLE Direct Submission				
JOURNAL Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK				
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Best Local Similarity	100.0%;	Pred. No. 2.9e-261;		
Matches 1602; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	285	GCGGTGTCTTCCGCCGCATGGTGCTCTGTCTCCTCATGGAAACAAGGCTCCACAAG	344
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QY	601	atcagatggtgtgtggtccttcttcaggcagttcttcaggtcagtcacccaaggttgactac	660
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QY	1141	gtgtggtagactctccagttctctctgtcagctatatatgaccttccccctctacgcgtcgtc	1200
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DEFINITION	Sequence 3 from Patent WO0078799.		linear
			PAT 24-JAN-2001

ACCESSION	AX063294
VERSION	AX063294.1
KEYWORDS	GI:12541084
SOURCE	Triticum sp.
ORGANISM	Triticum sp.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
AUTHORS	1 (bases 1 to 1868)
TITLE	Salmeron,J.M., Weislo,L.J., Strawn,L.J., Kramer,C.M., Wang,H.X., Vernoolf,B.T., Levin,J.Z., Hellefetz,P.B., Patton,D.A. and Que,Q.
JOURNAL	MLO-genes controlling diseases
FEATURES	Patent: WO 0078799-A 3 28-DEC-2000; Novartis AG (CH)
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QY	82 gtgctcgtgcgcctcctcatggaacacgagcctccaagaagctcggccatgtgtccagcac 141
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QY	1099	tgtaccacaac	gcagatcgggctgagcatcatgaaagtgtgtgtggygctagctctccag	1158
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DEFINITION	Triticum aestivum seven transmembrane-spanning protein (M1o2) mRNA,	linear PLN 26-AUG-2001
	complete cds.	
ACCESSION	AF361932	
VERSION	AF361932.1	GI:15290588
KEYWORDS		
SOURCE	bread wheat.	
ORGANISM	Triticum aestivum	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1730)	Devoto, A., Hartmann, A., Pfaffenell, P., Elliott, C., Simmons, C., Taramino, G., Goh, C.-S., Schulze-Lefert, P. and Panstruga, R.	Co-Evolution among intracellular domains and the C-terminus of the seven-transmembrane Mlo protein is suggested by a detailed computational analysis

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1730)
AUTHORS Elliott, C.E. and Schulze-Isferti, P.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
Center, Colney lane, Norwich NR4 7UH, UK
FEATURES Location/Qualifiers
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DEFINITION	AX063296	Sequence 5	from Patent WO0078799.		
ACCESSION	AX063296				
VERSION	AX063296.1	GI:12541086			

SOURCE ORGANISM	Trilicium sp.	Trilicium sp.
Trilicium sp.		
Trilicium sp.		

Poolidae; Triticeae; Triticum.

REFERENCE AUTHORS	1 (bases 1 to 1693)
Salmeron, J. M., Weislo, L. J., Strawn, L. J., Kramer, C. M., Wang, H. X., Vernool, B. T., Levin, J. Z., Helfetz, P. B., Patton, D. A. and Que, Q.	

TITLE Mlo-genes controlling diseases
JOURNAL Patent: WO 0078799-A 5 28-DEC-2000;

Novartis AG (CH)	Location/Qualifiers
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RESULT 8
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LOCUS AF384144
DEFINITION Triticum aestivum MLO protein mRNA, complete cds.
ACCESSION AF384144
VERSION AF384144.1 GI:14334166
KEYWORDS
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 1819)
AUTHORS Yu, L., Niu, J.-S., Ma, Z.-Q., Chen, P.-D. and Liu, D.-J.
TITLE Cloning, location and expression of MLO gene from wheat
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1819)
AUTHORS Yu, L., Niu, J.-S., Ma, Z.-Q., Chen, P.-D. and Liu, D.-J.

TITLE Direct Submission
JOURNAL Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
Nanjing Agricultural University, Nanjing, Jiangsu, China
FEATURES
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LOCUS
DEFINITION
Triticum aestivum seven transmembrane-spanning protein (Mlo1) mRNA,
partial cds.
ACCESSION
AF361933
VERSION
AF361933.1 GI:15290590
KEYWORDS
bread wheat.
SOURCE
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
AUTHORS
Devoto, A., Hartmann, A., Piffanelli, P., Elliott, C., Simmons, C.,
Taramino, G., Goh, C.-S., Schulze-Lefert, P. and Panstruga, R.
TITLE
Co-Evolution among intracellular domains and the C-terminus of the
seven-transmembrane Mlo protein is suggested by a detailed
computational analysis
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1399)
AUTHORS
Elliott, C.E. and Schulze-Lefert, P.
TITLE
Direct Submission
JOURNAL
Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
Center, Colney Lane, Norwich NR4 7UH, UK
FEATURES
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DEFINITION Sequence 12 from Patent WO9804586.
ACCESSION A92838
VERSION A92838.1 GI:6741374
KEYWORDS
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1635)
Panstruga, R. and Bueschges, R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
PLANTS
JOURNAL Patent: WO 9804586-A 12 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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QY	480	gaatygagagacagagaccactcctcttggaatacacagtttcgcaaatgatactctgcaggt	539
Db	610	GAAGTGGGAATTAGAGACCAACTCGTTGGAGTATCAGTTTCGCAAAACGATCCTTACGATT	669
QY	540	ccggttcacgcaaccagacgtcgttcgtgaagcgcaacctggygcctctccagcaacctg	599
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QY	600	catcagatggtgtgtgcctctctcagcgcaattcttcaagttcagttcacccaagtgtgacta	659
Db	730	GCTCAGATGGATTGTGGCGGTTCTTTCAGGCGAGTCTTTCGGGCTCTGTACCAAGGTGCACTA	789
QY	660	cctgaaccttgagggcaggttcatcaacgcgcattgttcgcaaaacagcaagttcgaact	719
Db	790	CCTGACCATTGCGGCAAGGCTTCATCAATGCGCATTTGTTCGCAAGATAGCAAGTTCGACTT	849
QY	720	ccaccaagtacatacaagaagtcgattggaagcagactcaaggtcgtcgtcgcatcagcct	779
Db	850	CCACAAATACATCAAGAGGTCATTAGAGGACGATTTCAAAGTTGTCGTTGGCATCAGCCT	909
QY	780	ccgcgtgtggtgtgtgcgatacctcaaccctctccttgacaatcaatggttgcaacgt	839
Db	910	CCCATTTGTGTTGTTCGCGCATCTTGTGCTCTTCCATTATCCAAAGGTTCCGACGCT	969
QY	840	catctggaattcttcatccctctcgtgatacctctgtgtgttgaaccaagtgtgagat	899
Db	970	TATCTGGATCTCTTTGTTCACCTCGTCATCCTCATGTTGGTTGGACAAAGCTGGAGAT	1029
QY	900	gatacatatgagatggtcccttgagatccaggaaccggtgcagcgtcatcaaggtggcccc	959
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QY	960	cgtggtcagcccgcaacaagttcttctgtgttccaccgccccgactggtgtccttctt	1019
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QY	1020	catcaccttgacgttgttccagaacgcgttccagatggtgcgcaattgtgtgacagrygc	1079
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QY	1080	caagcccggttgaagaaatgttaccacaacgcagatcggtgtgacatcatgaagtgt	1139
Db	1210	AACCCCTGGCCTGAAGAAATGCTCCATGAATAACATGGGCTTGAGTATCATGAAGTGT	1269
QY	1140	ggtggtgactagctctccagttctctctgcagctataatgaccttccccctctacgcgtcgt	1199
Db	1270	AGTGGGATATTTCATTCAAGTTCCTATGCAAGCTACAGCACCTTCCCTCTPACGCACCTGCT	1329
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RESULT	13
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DEFINITION	Oryza sativa Mlo (Mlo) mRNA, complete cds.
ACCESSION	AF388195
VERSION	AF388195.1 GI:14718603
KEYWORDS	.
SOURCE	Oryza sativa.
ORGANISM	Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE	Ehrhartoidae; Oryzeae; Oryza. 1 (bases 1 to 1894) Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D., Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.J. Isolation and characterization of Mlo homolog in rice Unpublished 2 (bases 1. to 1894)
TITLE	Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D., Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.J. Direct Submission Submitted (01-JUN-2001) Biochemistry, Gyeongsang National University, Gazwa-dong 900, Chinju 660-701, Korea
JOURNAL	location/Qualifiers
AUTHORS	1. .1894 /organism="Oryza sativa" /cultivar="MilYang 117"
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BASE COUNT	438 a 493 c 558 g 405 t
ORIGIN	

Query Match 50.8%; Score 813.4; DB 8; Length 1894;
Best Local Similarity 71.7%; Pred. No. 5.5e-128;
Matches 1188; Conservative 0; Mismatches 361; Indels 108; Gaps 5;

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Db 159 GGGAGGGCGCTTGGCCGAGACGGCGACGTGGGGCGGTGGCCGTCTCGCCGTCATCGT 218
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Db 1758 GTCGGCCGACATTCGCGATTGATTTCCTTCAGC 1794

RESULT 14
AY029312 1872 bp mRNA linear PLN 15-JUN-2001
LOCUS
DEFINITION Zea mays seven transmembrane protein M101 mRNA, complete cds.
ACCESSION AY029312
VERSION AY029312.1 GI:13784974
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 1872)
AUTHORS Briggs,S.P. and Simmons,C.R.
TITLE Manipulation of mlo genes to enhance disease resistance in plants
JOURNAL Patent: PCT WO/00/01722-B 07-JUL-1999;
REFERENCE
2 (bases 1 to 1872)
AUTHORS Cahoon,R.E., Miao,G.-H., Rafalski,J.A. and Taramino,G.
TITLE Zea mays cDNA encoding southern corn leaf blight resistance protein
JOURNAL Patent: PCT WO9923235-B 05-NOV-1999;
REFERENCE
3 (bases 1 to 1872)
AUTHORS Devoto,A., Hartmann,A., Piffanelli,P., Elliott,C., Simmons,C.R.,
Taramino,G., Goh,C.-S., Cohen,F.E., Schulze-Lefert,P. and
Panstruga,R.
TITLE Molecular phylogeny and domain-specific co-evolution of the
JOURNAL plant-specific seven transmembrane M10 family
REFERENCE unpublished
4 (bases 1 to 1872)

Db 1633 GAGGATGAGCCCGCTGCTCCACCGCGTCAACATGACATCGTGATGCGCATTTTTC 1692
OY 1587 ctccagccaggatga 1602
Db 1693 TTTAGCATGCGGTGA 1708

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A92837
LOCUS A92837 1611 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 11 from Patent WO9804586.
ACCESSION A92837
VERSION A92837.1 GI:6741373
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Panstruga, R. and Bueschges, R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
JOURNAL PLANTS
Patent: WO 9804586-A 11 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRU GA RALPH (GB)

FEATURES
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BASE COUNT 348 a 451 c 450 g 362 t
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Best Local Similarity 71.68; Pred. No. 3.6e-120;
Matches 1152; Conservative 0; Mismatches 383; Indels 75; Gaps 8;

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OY 467 tgagaacatggaagaatggtgagacagagaccactctcttgataaccagttcgcaatg 526
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Search completed: July 23, 2002, 09:37:03
Job time: 2196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:24:40 ; Search time 69 Seconds

(without alignments)
1336.323 Million cell updates/sec

Title: US-09-722-377-1

Perfect score: 2788

Sequence: 1 MSDKGVAPARELPETPSNAV.....ASSSALADIPSDPSFSQG 533

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2429	87.1	534	10 Q94F74	Q94F74 triticum ae
3	2411	86.5	534	10 Q94F71	Q94F71 triticum ae
4	2084	74.7	435	10 Q94F73	Q94F73 triticum ae
5	2049.5	73.5	555	10 Q95NKS	Q95NKS oryza sativ
6	2046.5	73.4	555	10 Q93XC8	Q93XC8 oryza sativ
7	1880	67.4	554	10 Q94EX3	Q94EX3 oryza sativ
8	1727	61.9	563	10 Q94CH4	Q94CH4 zea mays (m
9	1257	45.1	515	10 Q94CG9	Q94CG9 zea mays (m
10	1255.5	45.0	576	10 Q94KB3	Q94KB3 arbidopsi
11	1253.5	45.0	573	10 Q95XB6	Q95XB6 arbidopsi
12	1234.5	44.3	583	10 Q95Y94	Q95Y94 arbidopsi
13	1231.5	43.8	583	10 Q94KB7	Q94KB7 arbidopsi
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15	1160	41.6	565	10 Q94CH3	Q94CH3 zea mays (m
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19	1088	39.0	574	10 Q9SHM0	Q9SHM0 arbidopsi
20	1049	37.6	443	10 Q9C855	Q9C855 arbidopsi
21	961	34.5	508	10 Q94KB9	Q94KB9 arbidopsi
22	901	32.3	339	10 Q94KB4	Q94KB4 arbidopsi
23	888.5	31.9	406	10 Q94KB6	Q94KB6 arbidopsi
24	888.5	31.9	492	10 Q94CB7	Q94CB7 zea mays (m
25	888	31.9	478	10 Q94CB2	Q94CB2 arbidopsi
26	881	31.6	171	10 Q94CB8	Q94CB8 triticum ae
27	853.5	30.6	429	10 Q95TW9	Q95TW9 arbidopsi
28	804.5	28.9	554	10 Q94CB1	Q94CB1 arbidopsi
29	801.5	28.7	496	10 Q94CH2	Q94CH2 zea mays (m
30	790.5	28.4	485	10 Q94CB8	Q94CB8 arbidopsi
31	790	28.3	573	10 Q9F100	Q9F100 arbidopsi
32	783.5	28.1	499	10 Q94CG8	Q94CG8 zea mays (m
33	735.5	26.4	509	10 Q94CH1	Q94CH1 zea mays (m
34	712.5	25.6	573	10 Q94KB8	Q94KB8 arbidopsi
35	631	22.6	507	10 Q91QY2	Q91QY2 arbidopsi
36	614.5	22.0	311	10 Q94ON5	Q94ON5 arbidopsi
37	600.5	21.5	469	10 Q94CG6	Q94CG6 zea mays (m
38	274	9.8	103	10 Q9XJ52	Q9XJ52 triticum ae
39	243	8.7	149	10 Q94CH0	Q94CH0 zea mays (m
40	114	4.1	628	16 Q92F14	Q92F14 listeria in
41	108.5	3.9	389	4 Q9H618	Q9H618 homo sapien
42	107	3.8	1826	3 Q9P377	Q9P377 schizosacch
43	105	3.8	920	4 Q96PH5	Q96PH5 homo sapien
44	103.5	3.7	770	17 Q97U12	Q97U12 sulfolobus
45	103	3.7	712	10 Q94EK6	Q94EK6 pisum sativ

ALIGNMENTS

RESULT 1
Q94F72 PRELIMINARY; PRT; 534 AA.
ID Q94F72
AC Q94F72;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MLO PROTEIN.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT "Cloning, location and expression of MLO gene from wheat."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF384144; AAK60566.1; -
SQ SEQUENCE 534 AA; 60298 MW; 6C9640F30FDE5189 CRC64;

Query Match 87.3%; Score 2434; DB 10; Length 534;
Best Local Similarity 88.8%; Pred. No. 3.2e-225;
Matches 469; Conservative 22; Mismatches 33; Indels 4; Gaps 3;

QY 8 PARELPETPSMAVAVFAAMVLVSVMHGLHKLGHMFQHRHKKALWEALKKAEMLV 67
DB 9 PARTLPETPSMAVALVFAVMIIIVSVLLEHKLGHMFHKKHKKALAELEKKAEMLV 68
QY 68 GFISLLIVTQDPLIAKICISDADAVMPCRGTEGRKPSKYVDY--CPEGVALMSTG 125
DB 69 GFISLLAVTQDP-ISGICISQKAASIMRECK-VEPGSVSKYKDYICAKGKVALMSTG 126
QY 126 SLHQLHVFIFVLAVFHTVSVITIALSRKMKRTWKWETETTSLEYQFANDPARFRTHQ 185
DB 127 SLHQLHVFIFVLAVFHTVSVITIALSRKMKRTWKWETETTSLEYQFANDPARFRTHQ 186
QY 186 TSFVKRHLGLSSTPGIRNVVAFFROFERSVTKVDYLLTRAGFINAHLSONSKFDFHKYIK 245

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Db 187 TSFVKRHLGLSTPGVWVAFRRQFRSTKVDYLIRAGFINAHLSONSKFDFHKYIK 246
QY 246 RSMEDDFKVVVGISLPLMGVAITLTLFDINGVGTLLWISFIPVILLCVGTKLEIMEM 305
Db 247 RSMEDDFKVVVGISLPLMAVAITLTLFDIDIGITLWVSFIPVILLCVGTKLEIMEM 306
QY 306 ALEIODRASVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
Db 307 ALEIODRSSVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTVATPGLK 366
QY 366 KCYHTQIGLSIMKVVGALQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKALTWRN 425
Db 367 DCEHMNIGLSIMKVVGALQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKALTWRN 426
QY 426 TAKEKKKVRDITMLMAQMGIGDATPSRGSSPMPSPRGSSPVHLHKGMRSDDPQSAFTSPR 485
Db 427 TAKEKKKVRDITMLMAQMGIGDATPSRGSSPMPSPRGSSPVHLHKGMRSDDPQSAFTSPR 486
QY 486 TQOEARDMPVYVAHPVHRLNPNDRRRSASSALADIPSADFSFSOG 533
Db 487 TMEEARDMYPVVAHPVHRLNPADRRRSVSSALDADIPSADFSFSOG 534

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RESULT 2
ID 094FR4 PRELIMINARY; PRT: 534 AA.
AC 094FR4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SEVEN TRANSMEMBRANE-SPANNING PROTEIN.
GN MLO2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BOB WHITE;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.;
RT "Co-Evolution among intracellular domains and the C-terminus of the
RT seven-transmembrane MLO protein is suggested by a detailed
RT computational analysis.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361932; AAK94904.1; .
KW Transmembrane.
SQ SEQUENCE 534 AA; 60427 MW; 2DB2384078336D00 CRC64;

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Query Match 87.1%; Score 2429; DB 10; Length 534;
Best Local Similarity 88.0%; Pred. No. 9.6e-225;
Matches 469; Conservative 22; Mismatches 38; Indels 4; Gaps 3;
QY 3 DKKGVPAELPETPSMAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKKA 62
Db 4 DDEYPPARTLPETPSMAVALVFAVMITVSYLEHALHKLGHWFHKKRNALAELEKKA 63
QY 63 ELMVGFISLLIVTODPIAKICISEDADAVMPCCKRGTEGRKSKYVDY--CPEGKVA 120
Db 64 ELMVGFISLLAVTQDP-ISGICISEKAASIMRCKL-PPGSVSKYKDYCAKQKVS 121
QY 121 LMSTGSLHQLHVFIVLAVFHTYSVITIALSRKMKRTWKWETETTSLEYQFANDPARF 180
Db 122 LMSTGSLHQLHVFIVLAVFHTYSVITIALSRKMKRTWKWETETTSLEYQFANDPARF 181
QY 181 RFTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLRAGFINAHLSONSKFDF 240
Db 182 RFTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLRAGFINAHLSONSKFDF 241
QY 241 HKYIKRSMEDDFKVVVGISLPLMGVAITLTLFDINGVGTLLWISFIPVILLCVGTKLEM 300

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Db 242 HKYIKRSMEDDFKVVVGISLPLMGVAITLTLFDIDIGITLWVSFIPVILLCVGTKLEM 301
QY 301 IIMEMALEIODRASVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTV 360
Db 302 IIMEMALEIODRASVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTV 361
QY 361 TPGLKKCYHTQIGLSIMKVVGALQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKAL 420
Db 362 TPGLKKCFHMHIGLSIMKVVGALQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKAL 421
QY 421 TNNRNTAKEKKKVRDITMLMAQMGIGDATPSRGSSPMPSPRGSSPVHLHKGMRSDDPQSA 480
Db 422 TNNRNTAKEKKKVRDITMLMAQMGIGDATPSRGASPMPSRGSSPVHLHKGMRSDDPQST 481
QY 481 PTSPRTQOEARDMPVYVAHPVHRLNPNDRRRSASSALADIPSADFSFSOG 533
Db 482 PTSPRAMEARDMYPVVAHPVHRLNPADRRRSVSSALDADIPSADFSFSOG 534

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RESULT 3
ID 094F71 PRELIMINARY; PRT: 534 AA.
AC 094F71;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MLO1 PROTEIN.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT "Cloning, characterization analysis and expression of MLO1 gene from
RT wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF344145; AAK60567.1; .
KW SEQUENCE 534 AA; 60402 MW; 7CB1B6B64F3C5E66 CRC64;

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Query Match 86.5%; Score 2411; DB 10; Length 534;
Best Local Similarity 87.6%; Pred. No. 5.2e-223;
Matches 467; Conservative 22; Mismatches 40; Indels 4; Gaps 3;
QY 3 DKKGVPAELPETPSMAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKKA 62
Db 4 DDEYPPARTLPETPSMAVALVFAVMITVSYLEHALHKLGHWFHKKRNALAELEKKA 63
QY 63 ELMVGFISLLIVTODPIAKICISEDADAVMPCCKRGTEGRKSKYVDY--CPEGKVA 120
Db 64 ELMVGFISLLAVTQDP-ISGICPEKAASIMRCKL-PPGSVSKYKDYCAKQKVS 121
QY 121 LMSTGSLHQLHVFIVLAVFHTYSVITIALSRKMKRTWKWETETTSLEYQFANDPARF 180
Db 122 LMSTGSLHQLHVFIVLAVFHTYSVITIALSRKMKRTWKWETETTSLEYQFANDPARF 181
QY 181 RFTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLRAGFINAHLSONSKFDF 240
Db 182 RFTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLRAGFINAHLSONSKFDF 241
QY 241 HKYIKRSMEDDFKVVVGISLPLMGVAITLTLFDINGVGTLLWISFIPVILLCVGTKLEM 300
Db 242 HKYIKRSMEDDFKVVVGISLPLMGVAITLTLFDIDIGITLWVSFIPVILLCVGTKLEM 301
QY 301 IIMEMALEIODRASVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTV 360
Db 302 IIMEMALEIODRASVIKGAPEVPSNKFWEHRDPDWLFFIHLTLFQNAFQMAHFVWTV 361
QY 361 TPGLKKCYHTQIGLSIMKVVGALQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKAL 420

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Db 362 TRGLKCFMHMIGLSIMKVVGLALQFLCSYTFPLVALVTQMSNMKRSIFDEQAKAL 421
QY 421 TNWRMTAKEKKKVRDMDLMAOMIGDATPSRGSSPMPSSRGSSPVHLHKMGGRSDDPQA 480
Db 422 TNWRMTAKEKKKVRDMDLMAOMIGDATPSRGASPMPSRGSSPVHLHKMGGRSDDPQST 481
QY 481 PTSPTQOEARMYPVVAHVHRLNPNDRRRSASSALLEADIPSADFSFSG 533
Db 482 PTSPTQOEARMYPVVAHVHRLNPNDRRRSASSALLEADIPSADFSFSG 534

RESULT 4
ID Q94FR3 PRELIMINARY; PRT; 435 AA.
AC Q94FR3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SEVEN TRANSMEMBRANE-SPANNING PROTEIN (FRAGMENT).
GN MLO1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BOB WHITE;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.,
RT "Co-Evolution among intracellular domains and the C-terminus of the
RT seven-transmembrane Mlo protein is suggested by a detailed
RT computational analysis."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361933; AAK94905.1; -
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 435 AA: 49354 MW: 3D96BD52FA62D42B CRC64;

Query Match 74.7%; Score 2084; DB 10; Length 435;
Best Local Similarity 91.9%; Pred. No. 1.1e-191;
Matches 397; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

QY 104 GRKPSKYVDY--CPEGKVALMSTGSLHOLHFVFLAVFHVHTYSVTITIALSRKMTWK 161
Db 4 GSVKSKYKDYCAKEGKVALMSTGSLHOLHFVFLAVFHVHTYSVTITIALSRKMTWK 63
QY 162 WETETTSLEYQFANDPARFRTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYL 221
Db 64 WETETTSLEYQFANDPARFRTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYL 123
QY 222 TLRAGFINAHLSONSKDFHKKYIKRSMEDDFKVVVGSISLPLMGVAITLFLDINGVGLI 281
Db 124 TLRAGFINAHLSONSKDFHKKYIKRSMEDDFKVVVGSISLPLMGVAITLFLDINGVGLI 183
QY 282 WISFIPLVILLCVGCKLEMITMENAIEIQDRASVTKGAPVVERPSNKFEPHPRPDVLEFI 341
Db 184 WISFIPLVILLCVGCKLEMITMENAIEIQDRSSVTKGAPVVERPSNKFEPHPRPDVLEFI 243
QY 342 HLTFLQNAFQMAHFVWTATPGKCCYHTQIGLSIMKVVGLALQFLCSYTFPLVALVT 401
Db 244 HLTFLQNAFQMAHFVWTATPGKCCYHTQIGLSIMKVVGLALQFLCSYTFPLVALVT 303
QY 402 QMSNMKRSIFDEQTSKALTINMNTAKEKKKVRDMDLMAOMIGDATPSRGSSPMPSSRG 461
Db 304 QMSNMKRSIFDEQTSKALTINMNTAKEKKKVRDMDLMAOMIGDATPSRGSSPMPSSRG 363
QY 462 SPVHLHKMGGRSDDPQASAPTSPTQOEARMYPVVAHVHRLNPNDRRRSASSALLEA 521
Db 364 SPVHLHKMGGRSDDPQASAPTSPTQOEARMYPVVAHVHRLNPNDRRRSASSALLEA 423
QY 522 DIPSADEFSFSG 533

Db 424 DIPSADEFSFSG 435
RESULT 5
ID Q9SNK5 PRELIMINARY; PRT; 555 AA.
AC Q9SNK5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SIMILAR TO OSMLO-H1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 3, PAC
RT clone:P0043E01."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000615; BAA85400.1; -
DR InterPro: IPR004326; MLO.
DR Pfam: PF03094; MLO; 1.
SQ SEQUENCE 555 AA: 62685 MW: F651FADB3B79E13C CRC64;

Query Match 73.5%; Score 2049.5; DB 10; Length 555;
Best Local Similarity 72.1%; Pred. No. 3.1e-188;
Matches 403; Conservative 49; Mismatches 64; Indels 43; Gaps 8;

QY 6 GVPARELPETPSWAVAVFAAMVLSVMEHGLHKLGHWFQHRKKALKWALEKMAELM 65
Db 4 GGGGRALPETPWAVAVCAVIVSVAMEHGLHKLGHWFHKKREKKAMGEALIKALM 63
QY 66 LVGFISLLIYTDPIIAKICISEDADVMPPCK-----RTEGRKPSK-----YV--- 111
Db 64 LIGFISLLIYTAQTP-ISKICIPESANIMLPCKAGODIVKLGKCKDHRRLMYTGEE 122
QY 112 -----DYCEP-GKVALMSTGSLHOLHFVFLAVFHVHTYSVTITIALSRKMR 157
Db 123 ESHRSLAGAGEDYCAQSGKVALMSSGGMHQLHFVFLAVFHVHTYCVTLMALGRLKM 182
QY 158 TWKMWETETTSLEYQFANDPARFRTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTK 217
Db 183 KWKKWLETETTSLEYQFANDPARFRTHQTSFVKRHLGLSTPGIRWVVAFFRQFRSVTK 242
QY 218 VDYLTLRAGFINAHLSONSKDFHKKYIKRSMEDDFKVVVGSISLPLMGVAITLFLDINGV 277
Db 243 VDYLTMRQGINAHLSONSKDFHKKYIKRSLLEDDEKVVVGSISLPLMGVAITLFLDINGV 302
QY 278 GTLIWISFIPLVILLCVGCKLEMITMENAIEIQDRASVTKGAPVVERPSNKFEPHPRPDV 337
Db 303 GTLIWISFIPLVILLCVGCKLEMITMENAIEIQDRATVTKGAPVVERPSNKFEPHPRPDV 362
QY 338 LFFIHLTLFQNAFQMAHFVWTATPGKCCYHTQIGLSIMKVVGLALQFLCSYTFPL 397
Db 363 LFFIHLTLFQNAFQMAHFVWTATPGKCCYHTQIGLSIMKVVGLALQFLCSYTFPL 422
QY 398 ALVTQMSNMKRSIFDEQTSKALTINMNTAKEKKKVRDMDLMAOMIGDATPSRGSSPMP 457
Db 423 ALVTQMSNMKRSIFDEQTSKALTINMNTAKEKKKVRDMDLMAOMIGDATPSRGSSPMP 474
QY 458 SRGSSPVHLHKMGGRSDDPQASAPTSPTQOEARMYPVVAHVHRLNPNDRRR 512
Db 475 SRGSSPVHLHKMGGRSDDPQASAPTSPTQOEARMYPVVAHVHRLNPNDRRR 533
QY 513 SASSALADIPSADFSFSG 531
Db 534 SASSALADIPSADFSFSG 552

RESULT	6			
Q93XC8				
ID	Q93XC8	PRELIMINARY;	PRT;	555 AA.
AC	Q93XC8;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	SEVEN TRANSMEMBRANE PROTEIN MLO2.			
OS	Oryza sativa (Rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Emnartolidae; Oryzae; Oryza.			
OX	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. IRE64; TISSUE=LEAF;			
RA	Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,			
RA	Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;			
RT	"Molecular phylogeny and domain-specific co-evolution of the plant-			
RT	specific seven transmembrane MLO family.";			
RL	Submitted (May-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF384030; AAK94907.1; -.			
KW	Transmembrane.			
SQ	SEQUENCE	555 AA;	62655 MW;	F651FADB23E8683C CRC64;

Query Match	73.48;	Score 2046.5;	DB 10;	Length 555;
Best Local Similarity	72.18;	Pred. No. 5.9e-188;		
Matches 403;	Conservative 48;	Mismatches 65;	Indels 43;	Gaps 8;

QY	6	GVPARELPETPSNAVAVVFAAMVLYSVLMEHGLHKLGHMFQDRHKKALMEALEKKAKAELM	65
Db	4	GGGGRALPETPIWAVAVVCAVIVLYSVAMEHGLHKLGHMFHKKREKKAMGEALEKKAELM	63
QY	66	LVGFISLLIYQDPPIIAKICISEDADVMWPK-----RGTEGRKPSK-----YV---	111
Db	64	LLGFISLLIYAOTF-ISKICIPESAAINIMLPCKAGODIYKGLKGKKDHRRLMYTGE	122
QY	112	-----DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVITYSVITIALSRILKM	157
Db	123	ESHRRSLAGAGEDYCAOSGKVALMSSGGMHQLHIFIFVLAVFHVITYCVITMALGRILKM	182
QY	158	TWKKTETETTSLEYQFANDPARFRETHTQTSFVKRHLGLSSTPGCIRWVAEFRQFRSVTK	217
Db	183	KWKKELETNSLEYQFANDPSRFRHTQTSFVKRHLGLSSTPGLRWIVAFRQFRGSVTK	242
QY	218	VDYLLTRAGETNAHLSQNSKFDFHKYIKRSMEDDFKVYVVGISLPLMGVAILLTFLDINGV	277
Db	243	VDYLTMRQGETNAHLSQNSKFDFHKYIKRSLDEDDFKVYVVGISLPLMFVAILLVFLDIQGF	302
QY	278	GTLWISIFIPVLILCVGTKLEMIIMENALEIQDRASVIKGAVEREPSNKEFWFHRBDWV	337
Db	303	GTLWISFVPLVILMLVGTKLEMVIMEMAQEIQDRATVIKGAVEREPSNKYFWFNRBDWV	362
QY	338	LEFIHLTLFONAFOMAHFVMTVATPGLKCKYHTQIGLSIMKYVVGALQFLCSYMTFPLY	397
Db	363	LEFIHLTLFONAFOMAHFVMTLATPGLKCFHENMGLSIMKYVVGIFIQFLCSYSTFPLY	422
QY	398	ALVTOMGSNMKRSTFDEQTSKALTNNRNTAKKKKKVVRDITDMLAQMITGATPSRGSSPMP	457
Db	423	ALVTOMGSNMKRTFEBEQTMKALMMNRRTAREKKKLRLDADEFLAQMSGDT-----P	474
QY	458	SRGSSPVHLHLHKMGSRSDDPQSAPTSPRTQOEARDMPYVVA-----HPVHRLNPNDRRR	512
Db	475	SRGSSPVHLHLHKQVRSEDDPPSAPASBPGEAGEARDMYPVPVADVVRPHGFNRTDP-DKRR	533
QY	513	SASSSALADIPSDFSFS 531	
Db	534	AASSSAIQVDIADSDFSFS 552	

RESULT	7
Q94EX3	
ID	Q94EX3 PRELIMINARY; PRT; 554 AA.
AC	Q94EX3;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE	MLO.
GN	MLO.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartoideae; Oryzeae; Oryza.
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. MILYANG 117;
RA	Kim M.C., Lee S.H., Kim J.K., Chun H.J., Kim J.C., Heo W.D.,
RA	Chung W.S., Choi M.S., Park C.Y., Yoon H.W., Cho M.J.;
RT	"Isolation and characterization of Mlo homolog in rice.";
DR	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
SO	EMBL; AF388195; AAK72963.1; -.
SO	SEQUENCE 554 AA; 62454 MW; 029EAC3DBF80C847 CRC64;

Query Match	67.4%;	Score 1880;	DB 10;	Length 554;
Best Local Similarity	67.8%;	Pred. No. 6e-172;		
Matches 379;	Conservative 55;	Mismatches 81;	Indels 44;	Gaps 11;

QY	6	GVPARELPETPSMAVAVVEFAAMVLVSYLEMHEGLHKLIGHMPOHRHKKALWALEEKKAEIM	65
Db	4	GGGGRALPETPTMAVAVVCAVIVLVASAMEHGLHKLIGHMFKREKKAMGEALGKAEIM	63
QY	66	LVGFISLLIYTQDPIIAKICISEDADVMPCK-----RGTEGRKPSK-----YV---	111
Db	64	LLGFISLLIYAQTP-ISKICIPESANIMLPCAKGQDIYKGLGKKDHRRLMYTGEE	122
QY	112	-----DYCPE-GKVALMTSGSLHQHLHFIEYLAVFHYTYSVITIALSRUKMR	157
Db	123	ESHRRSLAGAGEDDYCAQSGKVALMTSGGMHQHLHIFIEYLAVFHYTVCVITMGLGRLKMK	182
QY	158	TMKKWETETTSLEYQFANDPARERFTHQTSFVKRHLG-LSTIPGIRWVAFFRQFFRSVT	216
Db	183	KWKKWEQTNLSLEYQFAIDPSRERFTHQTSFVKRHLGSESSITPLRWIVAFFRQFFRSVT	242
QY	217	KVDYLLTRAGFINAHLSONSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAITLPLEDING	276
Db	243	KVDYLLTRQGFINAHLSONSKDFDFHKYIKRSLDEDFKVVVGISLPLMGVILVLELDING	302
QY	277	VGTLIWISFPIVILLCVGTKLEIMIMALEIODRASVIKGA PVVERPSNKFEMHRPDM	336
Db	303	LGTLIWISFPLIIVLVGTKLEMIWQMAQEIQDRATVIOGAPVVERPSNKFEMWRPDM	362
QY	337	VLEFIHLTFONAFQMAHFVMTVATPGLKKCYHTQIGLSIMKVVGALQFLCSYMTPL	396
Db	363	VLEFIHLTLFNHAFQMAHFVMTMATPGLKCFHENIMWLSIEVIVGISLQVLCSYTPEPL	422
QY	397	YALVTOGMSNMKRSIFEDQTSKALTNNRNTAKKKKVVROTFDMLMAQMGDATPSRGSSPM	456
Db	423	YALVTOGMSNMKRTIFEEQTMKALMNMKKAAMEKKKVRBADAFLAQMSVDF-----ATPA	477
QY	457	PSRGSSPVHLHKMGSRDDPOSAPT--SPRTQOEARMYPVVVAHPVHRL--NPNDRRR	512
Db	478	SSRSASPVHLLODHRARLDDPPSPITVASPPAPEE--DIYVFAAAAFCQLDDPDRRW	535
QY	513	SASSSALADIPSADFSFS 531	
Db	536	MAS---LSADIPDEDFFSFS 551	

RESULT	8
Q94CH4	
ID	Q94CH4
PRELIMINARY;	
PRT;	563 AA.

AC 094CH4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SEVEN TRANSMEMBRANE PROTEIN MLO1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B73;
RA Briggs S.P., Simmons C.R.;
RT "Manipulation of mlo genes to enhance disease resistance in plants.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B73;
RA Cahoon R.E., Miao G.-H., Rafalski J.A., Taramino G.;
RT "Zea mays cDNA encoding southern corn leaf blight resistance
RT protein.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B73;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane Mlo family.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029312; AAK38337.1; -.
KW Transmembrane.
SO SEQUENCE 563 AA; 63086 MW; B021C891063FF03B CRC64;

[illegible]

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Db      480  TTPSHSRATSPSRGNSPVHLLHKYRGSRSEPOSGPASP--GREIGDMYPVADQRLRLRLD  537
      ||| : ||||:||||| |||::||| | || : ||||
QY      507  PNDRRRSASSSALEADIPSADFSFS  531
      | : | |||:| : || |||||
Db      538  P-ERMRRPASSTAVNIDIADADFSS  561

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RESULT	9
Q94CG9	
ID	Q94CG9
	PRELIMINARY;
	PRT; 515 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE SEVEN TRANSMEMBRANE PROTEIN MLO6.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. H11;
RA Briggs S.P., Simmons C.R.;
RT "Manipulation of mlo genes to enhance disease resistance in plants.";
RN [2]
RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. H11;
CAhoon R.E., Miao G.-H., Rafalski J.A., Taramino G.;
RT "Zea mays cDNA encoding southern corn leaf blight resistance
RT protein.";
RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. H11;
RA Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane Mlo family.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029317; AAK38342.1; -
KW Transmembrane.
SO SEQUENCE 515 AA; 56984 MW; 8C61F12E7C8A0D3B CRC64;

Query Match	45.1%;	Score 1257;	DB 10;	Length 515;
Best Local Similarity	48.7%;	Pred. No. 4.2e-112;		
Matches 251;	Conservative 84;	Mismatches 116;	Indels 64;	Gaps 7;

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QY      6 GVPARELPETPSNAVAVVEAAMVLVSVMENHGLKHLKGHWFOHRKKALMEALEKKMAELM   65
      1 : : | | : : | | | | | : : | : | : | : | : | : | : | | | | | | | |
Db     7 GGNSRELDOTPTMAVASVCGYIVLISILEKGLHHVGFEFFSHRKKKAAVEALEKKVAELM   66
QY     66 LVGEISLLIIVODPIIAKICISEDADVMWPCK-----RGTE-----    103
      ::| | | | | : : | | : | | | | : | | | | | | | | |
Db     67 VLGEISLLLVGQNYII-KVCISNHAANTMLPCKLEAAAVEGKHGKEAAAVAGKKKY    125
QY     104 -----GRKPSK-----YVDY-----CPEGKVALMSTGSLH    128
      : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db     126 AVAVPGKKKKKAAAADHLGGVNDWPPYYAHNARMLAEASMATKCPEGKVPLISINALH    185
QY     129 OLHFIFIVLAVERHYTVSITIALSR LKMRTWKMETETTSLXOFANDPARFRTHOTSF    188
      ||||:| | | | | | : | | : | | | | : | : | | | | | | | | | | | |
Db     186 QLHFIFFLAVERHSYSAITMALGRAKIRAWKEWEKEAAGODEEFSHDPTRFRTHTETSF    245
QY     189 VKRHIG-LSSTPGIRWVVAFFROFERSVTYKVDTLLRAGFINAHISQNSKDFHKYIKRS    247
      |::| : | : : | | | | | : | | | | : | : | | | | | | | | | |
Db     246 VRQHMTNLNKFPASFYISNFQRQFERSVQADYCALKRHSFVNHLAPGSKFDFQKIYKRS    305
QY     248 MEDDFKVVVGISILPMGVAILTLFLDINGVGLTIWISFIPLVILLCVGTKLEMIIMEMAL    307
      : | | | | | : | | | | : : | | : : | | : : | | : | | | | : | |
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Db 306 LEDDEKYIVGISPPLMASALIFELFLVNGWHTMLWISIMPVVILISVGTKLOGIICRMAI 365
QY 308 EIQDRASVIKGAVPVEPSNKFWEHRDVLFEIHLTFQNAFQMAHFVTVATPGLKKC 367
Db 366 DITERHAVIQGIPIVQVSDSYFEWARPFLVFLIHFTLFQNGFQIIFYFLMILYEGMDSC 425
QY 368 YHTQIGLSIMKVVVGLALQFLCSYMFEPALVLTQMGSMKRSIFDEQTSKALTNRNTA 427
Db 426 FNDSEEFVARLCLGVVQVLCSTYTLPLVALVSQMGSTMKOSIFDEQTSKALKNRAGA 485
QY 428 KEKKKVRDFTDMLMAQMGDATPSRGSSPMSRGSS 462
Db 486 KKKAPTTGG-----SKHGGGSGPTAGSGPTKADGDA 515
RESULT 10
Q94KB3 PRELIMINARY; PRT; 576 AA.
AC Q94KB3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MEMBRANE PROTEIN MLO12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane MLO family."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF369573; AAK53805.1; -.
SQ SEQUENCE 576 AA; 66548 MW; 43DA9F6AED64D8E6 CRC64;

Query Match 45.0%; Score 1255.5; DB 10; Length 576;
Best Local Similarity 46.0%; Pred. No. 6.7e-112;
Matches 258; Conservative 93; Mismatches 155; Indels 55; Gaps 11;

QY 7 VPARELPETPSMAVAVFAAMVLVSVMHEGLHKLGHWFQHRHKKALWEALEKMAELML 66
Db 3 IKERSLEETPTWAVAVVCFVLLFISIMIEFLHFIGHWEKKHKKALSEALEKVAELML 62
QY 67 VGFISLLIVTODPIIAKICISEDADVMWPCCKRGTE-----GRK----- 106
Db 63 LGFISLLVLTQTP-VSEICIPRNIAATWHPSCSNHQEIAKYGKDYIDGRKILEDFDSND 121
QY 107 -----PSKYVDYCPG-KGVNLMSTGSLHQLHVFIEVLAVFHVTVYSVITIALSRKMR 157
Db 122 FYSPPRNLAATKGYDKCAEKGVALVSAYGIHQHLHIFIVLAVFHVLYCIITYALGKTKMK 181
QY 158 TWKKWETETTSLEYOFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVAFFRQFRSVT 216
Db 182 KWKSWERETKTIYQYANDPERFRFARDTSGRRHLNIMWSKSTFTLWITCFEFGSVT 241
QY 217 KVDYTLTRAGFTINAHLSQNS--KDFEHKTYIKRSMEDDFKVVVGISLPLMGVAILLTFLDI 274
Db 242 KVDYTLTRHGFTMAHLPAAGSARFDFQKTIERSLEODFTVVVGISPLWCIAVLFIILTNT 301
QY 275 NGVGTLLWISFPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAVPVEPSNKFWEHRP 334
Db 302 HGWDSYLMPLPLPLVILIVGAKLQMTISKILRIQEKGDVVKGAPVVEGGDDLLFWGFRP 361
QY 335 DWLLEFIHLTLFQNAFQMAHFVTVATPGLKCYHTQIGLSIMKVVVGLALQFLCSYMTF 394
Db 362 RFILFLIHLVLTNAFQLAFFVWSTYEFTLNKCFHKKTEDIAIRITMGVLIQVLCSTYTL 421
QY 395 PLVALVTQMGSMKRSIFDEQTSKALTNRNTPAKEKKKVRDFTDMLMAQMGDATPSRGSS 454
|||||

Db 422 PLVALVTQMGTSMRPTIFNDRYANALKKWHHTAKKQTKHGS-----GSNPHSSRP 473
QY 455 PMPSSGSPVHLLHKMGSRDDPQ----SAPTSPRTQGEARDMYPVVVAHPVHRLNPDR 510
Db 474 TPTFHGNSPVHLLHNNRSLDQOTSFTASPSPPRFSDYSGOGH----GHQ-HFFDPESQ 528
QY 511 RRSASSALEADIPSADEFSS 531
Db 529 NHS-----YQREITDSEFSNS 544

RESULT 11
Q9SXB6 PRELIMINARY; PRT; 573 AA.
AC Q9SXB6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T28P6.4 PROTEIN (MEMBRANE PROTEIN MLO2).
GN T28P6.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
RT specific seven transmembrane MLO family."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007259; AAD4991.1; -.
DR EMBL; AF369563; AAK53795.1; -.
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; MLO; 1.
SQ SEQUENCE 573 AA; 65543 MW; 36FA911F8B1D94A6 CRC64;

Query Match 45.0%; Score 1253.5; DB 10; Length 573;
Best Local Similarity 44.1%; Pred. No. 1e-111;
Matches 261; Conservative 91; Mismatches 161; Indels 79; Gaps 13;

QY 1 MSDKGVPAELPETPSMAVAVFAAMVLVSVMHEGLHKLGHWFQHRHKKALWEALEKM 60
Db 1 MADQ--VKERTLEETSTWAVAVVCFVLLFISIVLEHSIHKIGTWFKKKHQAALFEALEKV 58
QY 61 KAEMLVGFISLLIVTODPIIAKICISEDADVMWPCCKRGTEGKPKS----- 109
Db 59 KAEMLIGFISLLITIGOTP-ISNICISQKVASSTMHPCSAAEAKKYGKKDAGKKDDGCG 117
QY 110 -----YV-----DYCPG-KGVNLMSTGSLHQLHVFIEVLAVFHVTV 144
Db 118 DKPGRLLLELAESYIHRSLATKGYDKCAEKGVAFVSAYGIHQHLHIFIVLAVVHVY 177
QY 145 SVITIALSRILKMTWKWETETTSLEYOFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
Db 178 CIYTVARGIKMTKWSWEETKTIYQYSNDPERFRFARDTSFGRHRLNFWSKTRVTLW 237
QY 204 VVAFFRQFRSVTKVDYTLTRAGFTINAHLS--QNSKDFEHKTYIKRSMEDDFKVVVGISLP 261
Db 238 IYCFRQFRGVSYTKVDYALRHGFTMAHFAPGNESRFDFRKYIQRSLEKDKFTVEISPV 297
QY 262 LMGVAILLFLDLINGVGTLLWISFIPVILLCVGTKLEMIIMEMALEIQDRASVIKGA 321
:| | | | | : : : : : | | | | | : | | | | |

Db 298 IWEVAVLELLTNSYGLRSYLMLPEIPLVILIVGTKLEVIITKGLRIQEKGDVYRGAPV 357
QY 322 VEPSNKFWEHHRPDWVLFHILHLFQNAFQMAHFVWTVATPGLKCYHTQIGLSIMKVWV 381
Db 358 VQPGDDLFWGFKPRFILFLHLVLTNAFQALAFWMSYEFENLNCFHESHTADVIRLVV 417
QY 382 GLAQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKALTNMWNTAKEKKVYRDTMLMA 441
Db 418 GAVVQILCSYVTLPLALVTQMGSKMKPTVENRVATALKWHHTAKNETK-----HG 470
QY 442 QMIGDTPSRGSSPMPSRGSSPVHLHKMGSRDDPQSAPTSPRTQGEARDMYVVAHP 501
Db 471 RHSGSNPFSSRPTPTHGSSPIHLHNNRS--VENYSPSPSPRYSGH-----GHH 521
QY 502 VHRL-NPNDRRSASSS-----ALEADIP-----SADFSFSQ 532
Db 522 EHQFWDPESQHOEAETSTHSLAHESSEPVLASVELPPIRTSKSLRDFSFKK 573

RESULT 12
Q9SY94 PRELIMINARY; PRT; 583 AA.
AC Q9SY94;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T25B24.9 PROTEIN.
GN T25B24.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Federici N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shin P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC005850; AAD2552.1; -.
DR InterPro: IPR004326; MLO.
DR Pfam: PF03094; MLO.1.
SQ SEQUENCE 583 AA; 67226 MW; E6A3683CA8BB9150 CRC64;

Query Match 44.3%; Score 1234.5; DB 10; Length 583;
Best Local Similarity 43.6%; Pred. No. 7.2e-110;
Matches 261; Conservative 97; Mismatches 159; Indels 81; Gaps 12;
QY 1 MSDKKGVPARELPETPSNAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKM 60
Db 1 MADQ--VKEKLTETSTWAVAVCVFVLLISIVIEKLIHKIGSWFKKKKKKALYEALKEV 58
QY 61 KAEIMLVGFISLLIVTQDPIIAKICISEDADVMPCKRGTEGRK----- 106
Db 59 KAEIMLMGFISLLTIGQG-YISNICIPKNIASMHPCASASEARKYGGKDYPKDEEEN 117
QY 107 -----PSKYVDYCPG-GKVALMSTGSLHQLHVFIFVLAHFVHTYSVI 147
Db 118 LRRKLLQVDSLIPRSLATKGYDKCAEKGKVAFAVSAVGMHQLHIFIFVLAACHVYICV 177
QY 148 TIALSRKMRWKWKWETETTSLEYOFANDPARFRFTQTSFVKRHLGLSTPGIR-WVVA 206
Db 178 TYALGKTKMRWKWKEETKTIEYQSHDPERFRFARDTSFGRHRLSFWSKSTTLWIVC 237
QY 207 FFRQFRSVTKVDYLTLRAGFINAHLSONS--KFDHFHYIKRSMEDDFKVVVGISLPLWG 264
Db 238 FFRQFRSVTKVDYLTLRHGFIMAHLAGSDARFDFRKYIORSLEEDFKTIVEINPVIWF 297
QY 265 VALTLFLDINGVGTLIWISFPIVILLCVGTKLEMIIMEMALEIODRASVIKGAPEVP 324

Db 298 IAVLELLTNTNGLSYLMWLPFIPEIVILIVGTGLQVITITKGLRIQEKGDVYKGTPLVQ 357
QY 325 SNKFWEHHRPDWVLFHILHLFQNAFQMAHFVWTVATPGLKCYHTQIGLSIMKVWVLA 384
Db 358 GDHFEWGRPRFILFLHLVLTNAFQALAFWMSYERGLKNCFHESRVDTIRISIGLL 417
QY 385 LQFLCSYMTFPLALVTQMGSNMKSIFDEQTSKALTNMWNTAKEKKVYRDTMLMAQMI 444
Db 418 VQILCSYVTLPLALVTQMGSKMKPTVENRVATALKSWHHTAKNIKHGRTS----- 470
QY 445 GDATPSRGSSPMPSRGSSPVHLH--HKMGSRDDPQSAPTSPR-----TQGEA 490
Db 471 ESTTPFSSRPTPTHGSSPIHLHNAHPHKRSRVSDESFANSFSFRNSDFDSWDPESQHET 530
QY 491 RDMYPVVAHPVH--RLNPNDRRSASSALE-----ADIPSADFSFSQ 532
Db 531 AE-----TSNSNHRSRFGEESSEKRVSSVELPPGPGQIRTOHEISTISLRDFSFR 583

RESULT 13
Q94KB7 PRELIMINARY; PRT; 583 AA.
AC Q94KB7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MEMBRANE PROTEIN MLO6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the plant-
specific seven transmembrane MLO family."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF369567; AAK53799.1; -.
SQ SEQUENCE, 583 AA; 67097 MW; 4DA8683CA8BC5C5D CRC64;

Query Match 43.8%; Score 1221.5; DB 10; Length 583;
Best Local Similarity 43.5%; Pred. No. 1.3e-108;
Matches 260; Conservative 97; Mismatches 160; Indels 81; Gaps 12;
QY 1 MSDKKGVPARELPETPSNAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKM 60
Db 1 MADQ--VKEKLTETSTWAVAVCVFVLLISIVIEKLIHKIGSGFKKKKKKALYEALKEV 58
QY 61 KAEIMLVGFISLLIVTQDPIIAKICISEDADVMPCKRGTEGRK----- 106
Db 59 KAEIMLMGFISLLTIGQG-YISNICIPKNIASMHPCASASEARKYGGKDYPKDEEEN 117
QY 107 -----PSKYVDYCPG-GKVALMSTGSLHQLHVFIFVLAHFVHTYSVI 147
Db 118 LRRKLLQVDSLIPRSLATKGYDKCAEKGKVAFAVSAVGMHQLHIFIFVLAACHVYICV 177
QY 148 TIALSRKMRWKWKWETETTSLEYOFANDPARFRFTQTSFVKRHLGLSTPGIR-WVVA 206
Db 178 TYALGKTKMRWKWKEETKTIEYQSHDPERFRFARDTSFGRHRLSFWSKSTTLWIVC 237
QY 207 FFRQFRSVTKVDYLTLRAGFINAHLSONS--KFDHFHYIKRSMEDDFKVVVGISLPLWG 264
Db 238 FFRQFRSVTKVDYLTLRHGFIMAHLAGSDARFDFRKYIORSLEEDFKTIVEINPVIWF 297
QY 265 VALTLFLDINGVGTLIWISFPIVILLCVGTKLEMIIMEMALEIODRASVIKGAPEVP 324
Db 298 IAVLELLTNTNGLSYLMWLPFIPEIVILIVGTGLQVITITKGLRIQEKGDVYKGTPLVQ 357
QY 325 SNKFWEHHRPDWVLFHILHLFQNAFQMAHFVWTVATPGLKCYHTQIGLSIMKVWVLA 384

Db 358 GDHFWEGRPREFILHLVLTNAFQLAFFVWSTYEFGLKNCFHESRYDVIIRISIGL 417
QY 385 LQFLCSYMTFPLVALVTOMGSMNRKSFIDEOTSKALTNWRNTAKEKKVVDMLMAOMI 444
Db 418 VQILCSYVTLPLVALVTOMGSMKPTVFENERVATALKSMHTAKNIKHGRTS----- 470
QY 445 GDATPSRGSSPMPSRGSSPVHL-----HKMGSRDDPOSAPTSPR-----TQOEA 490
Db 471 ESTTPSSRPTPTTHGSSPIHLRNAPHKRSKSVDESFA NSFSPRNSDFDSWDPE SQHET 530
QY 491 RDMYPPVVAHPVH--RLNPNDRRRSASSALE-----ADIPSADFSFSQ 532
Db 531 AE-----TSNSNHRSRFGEESSEKKFVSSVLELPPGQIRTOHEISTISLRDESFKR 583

RESULT 14

Q9FRJ3 PRELIMINARY; PRT; 580 AA.
AC Q9FRJ3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE MLO (PATHOGEN RESISTANCE) PROTEIN.
GN OSJNB0064P21.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buehl C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujit C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0064P21 genomic sequence.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073166; AAC46114.1; -
SQ SEQUENCE 580 AA; 64796 MW; CD263AD8F8C350FC CRC64;

Query Match 42.8%; Score 1192; DB 10; Length 580;
Best Local Similarity 47.1%; Pred. No. 8.6e-106;
Matches 253; Conservative 80; Mismatches 146; Indels 58; Gaps 10;

QY 6 GVPARELPETPSNAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALMEALEKKAELM 65
Db 14 GDGARALDQPTNAVAACAVIVAASILEGLHHLGOWFSKRRKALFDALKEKXSELM 73
QY 66 LVGFISLLIVTQDPIIAKICISEDADAVMPCK-----RTEGRK-----PS 108
Db 74 TLGFISLLSVT--GRYISRICIPVGAADTMPCSLRSSSEQEVPGGGHGRRLSGDPT 132
QY 109 KYVDYCEPGKVALMSTGSLHQLHVFIFVLAHFVHTYVITIALSRKMRWKWETETTS 168
Db 133 NF--KCAKGMVSLVSADGLHQLHIFVFFLAHFVHSAITMSLGRAKTRIMKEKETCS 190
QY 169 LEYQFANDPARFRTHOTSFKVRLGL--SSTPGIRWVVAFFRQFRSVTKVDYLLRAGF 227
Db 191 LTYEFSDPSKFRLLTHOTSFVRQHASCSWSKSTITLYVFSFRQFRSVRRTDYLLRHGF 250
QY 228 INAHLSQNSKDFHKKYIKRSMEDDFKVVVGLSLPLMGVAITLFLDINGVGLIWISFIP 287
Db 251 IAAHLSLGTRENFRRYIKRSLDEDFKTVVGLSAPLWASALAIMLFNVHGMHNLFWESTIP 310
QY 288 LVLLCVGTKLEIMEMALEIODRASVYKGAPEVPSNKEFWHRPDWVLFHLLTLFQ 347
Db 311 LVVTLAVGTKLQAITAMAAVEIKERHTVIOGMPVVKLSDEHFWEGKPRVLVLIHFASFQ 370
QY 348 NAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTOMGSM 407

Db 371 NAFETTYFWIWEFGLRSCFHDNFELLIAVCLGVVVOFMCYITLPLVALVSQMSQM 430
QY 408 KRSIFDEQTSKALTNWRNTAKEKKVR-----DTDMLMAQMIGDATPSRGS 453
Db 431 KRIFDEQTAALKKWKAAVVKKQKSSHEPGSETPGTETTTTATATEESQREDA 490
QY 454 SPMSRGSSPVHL-----LHKG-----MGRSDDPOSAPTS--PTQOEAR 492
Db 491 AAMPVR-----HLHRYKTLAHVGATGTLSDSDCSDTDTPFASPTRLILPTKQRLD 542

RESULT 15

Q94CH3 PRELIMINARY; PRT; 565 AA.
AC Q94CH3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SEVEN TRANSMEMBRANE PROTEIN MLO2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. B73;
RA Briggs S.P., Simmons C.R.;
RT "Manipulation of mlo genes to enhance disease resistance in plants.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029313; AAK38338.1; -
KW Transmembrane.
SQ SEQUENCE 565 AA; 64278 MW; ADEA5EE7331F7407 CRC64;

Query Match 41.6%; Score 1160; DB 10; Length 565;
Best Local Similarity 44.5%; Pred. No. 9.9e-103;
Matches 253; Conservative 81; Mismatches 174; Indels 60; Gaps 11;

QY 6 GVPARELPETPSNAVAVFAAMVLSVLMHGLHKLGHWFQHRHKKALMEALEKKAELM 65
Db 3 GDGTALDQPTNAVAACAVIVAASILEGLHHLGQLLNKKRKAALFDALKEKXSELM 62
QY 66 LVGFISLLIVTQDPIIAKICISEDADAVMPCK-----RTEGRK-----PSKY 110
Db 63 TLGFISLLSVT--GRYIARICIPVGAADTMPCSLRSSSEQEVPGGGHGRRLSGDPTNL 120
QY 111 VDYCEPGKVALMSTGSLHQLHVFIFVLAHFVHTYVITIALSRKMRWKWETETTSLE 170
Db 121 FS-CRKGMVSLVSADGMHQLHIFVFFLAHFVHSAITMSLGRAKTRIMKEKETCSPO 179
QY 171 YQFANDPARFRTHOTSFKVRLGLSSTPGIR--WVAFFRQFRSVTKVDYLLRAGFIN 229
Db 180 YNYLNDPSKFRLLTHOTSFVRQHASCSWSKSTITLYVFSFRQFRSVRRTDYLLRHGFIS 239
QY 230 AHSLSQNSKDFHKKYIKRSMEDDFKVVVGLSLPLMGVAITLFLDINGVGLIWISFIP 289
Db 240 AHSLSLGTRENFRRYIKRSLDEDFKTVVGLSAPLWASALAVMLFNVHGMHNLFWESAIPLV 299
QY 290 ILLCVGTKLEIMEMALEIODRASVYKGAPEVPSNKEFWHRPDWVLFHLLTLFQ 349
Db 300 VILAVGTKLQAITAMAAVEIAERHTVIOGMPVVKLSDDHFWEGKPRVLVLIHFASFQ 359
QY 350 FQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTOMGSM 409

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2002, 14:25:25 ; Search time 25.02 Seconds

(without alignments)
824.841 Million cell updates/sec

Title: US-09-722-377-1

Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSALEADIPSADSFSG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2788	100.0	533	1 MLO_HORVU	P93766 hordeum vul
2	1941	69.6	544	1 MLH1_HORVU	O49873 hordeum vul
3	1792	64.3	537	1 MLH1_ORYSA	O49914 oryza sativ
4	1220.5	43.8	570	1 YML6_ARATH	O80961 arabidopsis
5	1101.5	39.5	501	1 MLO5_ARATH	O22815 arabidopsis
6	1061	38.1	580	1 YML1_ARATH	O22752 arabidopsis
7	1039	37.3	560	1 YML2_ARATH	O22757 arabidopsis
8	932.5	33.4	526	1 MLO1_ARATH	O49621 arabidopsis
9	927	33.2	496	1 ML15_ARATH	O80580 arabidopsis
10	499.5	17.9	447	1 YML3_ARATH	O23693 arabidopsis
11	429	15.4	217	1 YML4_ARATH	O81785 linum usita
12	102.5	3.7	574	1 YHGE_ECOLI	P45804 escherichia
13	95.5	3.4	443	1 HSLD_HELPJ	O92171 heliobacte
14	95.5	3.4	506	1 NFIC_PIG	P21999 sus scrofa
15	94.5	3.4	338	1 YD49_THEMA	O92170 thermotoga
16	94	3.4	395	1 Y306_MYCPN	P75343 mycoplasma
17	93.5	3.4	339	1 STEA_HUMAN	Q9uh88 homo sapien
18	93.5	3.4	369	1 Y316_MYCGE	P47558 mycoplasma
19	93.5	3.4	443	1 HSLD_HELPJ	O25254 heliobacte
20	93	3.3	1278	1 NPCL_HUMAN	O15118 homo sapien
21	92.5	3.3	262	1 COX3_ANOGA	P34842 anopheles g
22	92.5	3.3	262	1 COX3_DROYA	P00418 drosophila
23	92.5	3.3	439	1 NFIC_MOUSE	P70255 mus musculu
24	92	3.3	2376	1 YIM9_YEAST	P40468 saccharomyc
25	91.5	3.3	262	1 COX3_DROME	P00417 drosophila
26	91	3.3	439	1 IOLE_BACSV	P42417 bacillus su
27	91	3.3	762	1 AVP3_HORVU	O06572 hordeum vul
28	90.5	3.2	508	1 NFIC_HUMAN	P08651 homo sapien
29	90.5	3.2	1203	1 YTA1_CAEEL	Q11069 caenorhabdi
30	89.5	3.2	3079	1 IRA2_YEAST	P19158 saccharomyc
31	89	3.2	348	1 FMLI_GORGO	P79177 gorilla gor
32	89	3.2	1407	1 CYAA_DICDI	Q03100 dictyosteli
33	88.5	3.2	838	1 P_HUMAN	Q04671 homo sapien

34	88.5	3.2	970	1 Y277_MYCGE	O49409 mycoplasma
35	88	3.2	564	1 Y61A_MYCPN	P75041 mycoplasma
36	87.5	3.1	351	1 FMLI_HUMAN	P25090 homo sapien
37	87.5	3.1	568	1 PTLB_STRMU	P50976 streptococc
38	87.5	3.1	587	1 T9S3_MOUSE	O9et30 mus musculu
39	87	3.1	1012	1 DPOL_HSV7J	P52342 human herpe
40	87	3.1	1333	1 YN99_YEAST	P53756 saccharomyc
41	87	3.1	1835	1 CCAI_RAT	O920y8 rattus norv
42	86.5	3.1	348	1 FMLI_PONPY	P79236 pongo pygma
43	86.5	3.1	589	1 T9S3_HUMAN	O9hd45 homo sapien
44	86	3.1	384	1 AAPM_RHILV	O52814 rhizobium l
45	86	3.1	622	1 AMT3_CAEEL	Q21565 caenorhabdi

ALIGNMENTS

RESULT	ID	STANDARD	PRT	533 AA
MLO_HORVU	P93766;			
AC	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	MLO protein.			
GN	MLO.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.			
RC	STRAIN-VARIOUS STRAINS; TISSUE=Leaf;			
RX	MEDLINE=97207016; PubMed=9054509;			
RA	Bueschges R., Hollricher K., Panstruga R., Simons G., Wolter M.,			
RA	Frijters A., van Daelen R., van de Lee T., Diergaarde P.,			
RA	Groenendijk J., Toepesch S., Vos P., Salamini F., Schulze-Lefert P.;			
RT	"The barley Mlo gene: a novel control element of plant pathogen			
RT	resistance.";			
RL	Cell 88:695-705(1997).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV. INGRID;			
RX	MEDLINE=98128007; PubMed=9461468;			
RA	Panstruga R., Bueschges R., Piffanelli P., Schulze-Lefert P.;			
RT	"A contiguous 60 kb genomic stretch from barley reveals molecular			
RT	evidence for gene islands in a monocot genome.";			
RL	Nucleic Acids Res. 26:1056-1062(1998).			
CC	- FUNCTION: MAY BE INVOLVED IN DOWN-REGULATING LEAF CELL DEATH AND			
CC	PATHOGEN DEFENSE FUNCTIONS.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein (potential).			
CC	- MISCELLANEOUS: REF.1 HAS SEQUENCED MLO IN STRAINS CV. CARLSBERG			
CC	IT, CV. DIAMANT, CV. FOMA, CV. HAISA, CV. INGRID, CV. MALTERIA			
CC	HEDA, AND CV. PLENA.			
CC	- SIMILARITY: BELONGS TO THE MLO FAMILY.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; Z83834; CAB06083.1; -			
DR	EMBL; Y14573; CAA74909.1; -			
DR	Mendel; 13060; HORVU;2260;1.			
DR	InterPro; IPR004326; MLO.			
DR	Pfam; PF03094; MLO; 1.			
KW	Transmembrane; Pathogenesis-related protein.			
FT	TRANSMEM 18 38 POTENTIAL.			
FT	POTENTIAL. 63 83			


```
RESULT 3
MLH1_ORYSA
ID MLH1_ORYSA STANDARD: PRT: 537 AA.
AC 049914;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MLO protein homolog 1.
GN MLO-H1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. IR-BB21;
RA Panstruga R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
-----
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-----
CC
CC EMBL; 295353; CAB08606.1; -
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; Mlo; 1.
KW Transmembrane.
FT TRANSMEM 17 37 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 140 160 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 381 401 POTENTIAL.
SQ SEQUENCE 537 AA; 60077 MW; EE16772A9637416B CRC64;

Query Match 64.3%; Score 1792; DB 1; Length 537;
Best Local Similarity 67.2%; Pred. No. 3.4e-143;
Matches 366; Conservative 54; Mismatches 85; Indels 40; Gaps 12;

QY 9 ARELPETPSWAVAVFAAMVLYSVLMEHGLHKGHWFOHRHKKALWEAL---EKMAEL. 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 8 SRELPEPTWAVAVCAVLVLSAMEHGLHNLH-----KTTAEVLIFVLALAE. 60
QY 65 MLVGFISLLIVTQDPIIAKICISDAADVMWPKRGTE-----GRKPSKYV--DY 113
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 MLGFISLLITVAQAP-ISKICIPKSAANILLPCAGQDAIEEELASGRKSLAGAGGDY 119
QY 114 CP--EGKVALMSTGSLHQLHVEIFVLAHFVHTYSVTIALSRLLKMRWKWETETSL 171
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 120 CSKFDGKVALMSAKSMHQLHIFIVLAHFVHTYCIITMGLGRLLKMKWKWESQTSLE 179
QY 172 QFANDPARFRTHQTSFVKRHLG-LSTPGIRWVVAFFRQFFRSYTKVDYLTLAGAFIN 230
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 180 QFAIDPSRFRTHQTSFVKRHLSGFSSTPGIRWIVAFRQFFGSYTKVDYLTMRQFIN 239
QY 231 HLSQNSKDFHXYIKRSMEDDFKVVVGISLPLMGVAITLFLDINGVGLTIWISFPLVI 290
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 240 HLSQNSKDFHXYIKRSLDEDFKVVVGISLPLMGVILVLFIDHIGLGLTIWISFVPLI 299
QY 291 LLCVGTKLEMIIMALEIODRASVIKGAPEVPSNKEFWFHRPDWVLFPIHLTLFQNAF 350
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 300 VLLVGTKLEMIIMALEIODRASVIKGAPEVPSNKEFWFHRPDWVLFPIHLTLFHN 359
QY 351 QMAHFVWTVAATPGILKKCYHTQIGLSIMKVVVGIALQFLCSYMTFPLALVTQMG 410
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Db 360 QMAHFVWTVAATPGILKKCFHENIMWISIVEIVIGISLQVLCSYITFPLALVTQMG 419
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 411 IFDEQTSKALTNRNTAKEKKKVRDMDLMAOMIGDAPSRGSSPMPSRGSPVHLHKG 470
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 420 IFEEQTMKALMNRKKAMEKKKVRADAFLAQMSYDF-----ATPASSRSASPVHLQDH 474
QY 471 MGRSDDPGSAPT--SPRTQOEARMYPPVVAHPVHRL--NPNDRRRSASSALADIPSA 526
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 475 RARSDDPSPFITVASPPAPEE--DMTFVPAALASRQLDDPPDRMMASSS---ADIADS 529
QY 527 DFSFS 531
|||||
DB 530 DFSFS 534
```

```
RESULT 4
YML6_ARATH
ID YML6_ARATH STANDARD: PRT: 570 AA.
AC 080961;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical MLO-like protein At2g39200.
GN AT2G39200 OR T16B24.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Buell C.R., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
-----
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-----
CC
CC EMBL; AC004697; AAC28997.1; -
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; Mlo; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 156 176 POTENTIAL.
FT TRANSMEM 273 293 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
FT TRANSMEM 357 377 POTENTIAL.
FT TRANSMEM 400 420 POTENTIAL.
SQ SEQUENCE 570 AA; 65765 MW; 4C49EBF806F90910 CRC64;

Query Match 43.8%; Score 1220.5; DB 1; Length 570;
Best Local Similarity 45.3%; Pred. No. 4.7e-95;
Matches 254; Conservative 93; Mismatches 153; Indels 61; Gaps 12;
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ID	YMLL_ARATH	STANDARD	PRT	580 AA.
AC	022752;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical MLO-like protein At2g17430.			
GN	AT2G17430 OR F5J6.19.			
OS	Arabidopsis thaliana (Mouse-ear cross).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OX	eurosis II; Brassicales; Brassicaceae; Arabidopsis.			
NCBI_TaxID=3702;				
[1]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. COLUMBIA;			
RA	MEDLINE-20083487; PubMed-10617197;			
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,			
RA	Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,			
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,			
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,			
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,			
RA	Venter J.C.;			
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis			
RT	thaliana.";			
RL	Nature 402:761-768(1999).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- SIMILARITY: BELONGS TO THE MLO FAMILY.			
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CC	-----			
DR	EMBL; AC002329; AAB86520.2; -.			
DR	InterPro; IPR004326; MLO.			
DR	Pfam; PF03094; MLO; 1.			
KW	Hypothetical protein; Transmembrane.			
FT	TRANSMEM 39 59 POTENTIAL.			
FT	TRANSMEM 62 82 POTENTIAL.			
FT	TRANSMEM 196 216 POTENTIAL.			
FT	TRANSMEM 258 278 POTENTIAL.			
FT	TRANSMEM 319 339 POTENTIAL.			
FT	TRANSMEM 346 366 POTENTIAL.			
FT	TRANSMEM 445 465 POTENTIAL.			
SEQUENCE	580 AA; 66723 MW; AEF812A531E7EDAF CRC64;			
Query Match	38.1%; Score 1061; DB 1; Length 580;			
Best Local Similarity	45.7%; Pred. No. 1.3e-81;			
Matches 220; Conservative	75; Mismatches 130; Indels 56; Gaps 8;			
OY	6 GVPA-RELPEPPSWAVAVVFAAMVLVSIMEHGLKLGH-----	43		
DB	25 GAPSGKELSGPTWAVAVVCTFLILSHLEKGLQRLANVCFLLLLFLRVLEFKHSL	84		
OY	44 -----WFOHRHKKALMEALEKMKAEIMLVGFSILLIVTQDPIAKICISEDAD	93		
DB	85 SETYEFVSSQWLMMKKHNSLLEALEKIKAEIMLVGFSILLIVTQDPIAKICISEDAD	143		
OY	94 VMWPC-KRGT---EGRRKPSKYVDY-----CPEGKVALMSTGSLHQLVFIYVLAV	139		
DB	144 SMLPCLSEDIYVLEQKLAPSSLSRHLIAAGDTISNCKOGSEPLITLKGHLHLLFLAI	203		
OY	140 FHVTYSVTITIALSRLMKMTWKWETETTSLEYOFANDPARFRFTHTSFEVKKHGL-SST	198		
DB	204 FHIVYSLITMTLSRIKIRGWKKWEQETLSNDYEFSDHSRLRLTHETSFVREHTSFWT	263		

OY	199	PGIRWVAAFFROFFERSVT	KVDYLLTRAGFINAHL	SÖNSKEDFNHYIKRSM	EDDEKVVVG	1	258
		:	:	:	: :		
Db	264	PEFFYVGCFFRQFEVS	VERTDYLLTRHGFI	SAHLAPGRKFNQRYIKR	SLDEDEKLVGI	1	323
OY	259	SLPLMGVAILLFFEL	DINGVGTLLIWISFI	PVILLCVG	TKLEMIEMAL	EIQDRA	318
		:	: :	:	:	: :	
Db	324	SPVLMASEVILLEN	VNWGMRTLFWASIP	LLIILAVG	TKLQAINATMA	LEIVETHA	383
OY	319	APVVERPSNKEFW	HRPDVLFIFHLTL	FQNAFQMAHE	VWTVAPGLK	KCYHTQIG	378
		: :	: :	: :	: :	: :	
Db	384	MPLVQGS	DRYFEMDCPQ	LLHLHLHFAL	FQNAFOITHE	FWIMWSE	443
OY	379	VVVG	LALQFLCS	IMTFPL	YALVT-----	QMSNMKRS	430
		: :	:	:	:	:	
Db	444	LFLCL	GALILCS	ITLPL	YALVTO	MMKWCVEQ	503
OY	431	K	431				
Db	504	K	504				

RESULT	7		
ID	YML2_ARATH	STANDARD;	PRT; 560 AA.
AC	022757;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Hypothetical MLO-like protein At2g17480.		
GN	AT2G17480 OR MJB20.4 OR F5J6.23.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. COLUMBIA;		
RX	MEDLINE=20083487; PubMed=10617197;		
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,		
RA	Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,		
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,		
RA	Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,		
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,		
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,		
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,		
RA	Venter J.C.;		
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis		
RT	thaliana."		
RL	Nature 402:761-768(1999).		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC	-I- SIMILARITY: BELONGS TO THE MLO FAMILY.		
CC	-----		
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AC002329; AAB86524.1; -.		
DR	InterPro; IPR004326; MLO.		
DR	Pfam; PF03094; MLO; 1.		
KW	Hypothetical protein; Transmembrane.		
FT	TRANSMEM 12 32	POTENTIAL.	
FT	TRANSMEM 47 67	POTENTIAL.	
FT	TRANSMEM 93 113	POTENTIAL.	
FT	TRANSMEM 182 202	POTENTIAL.	
FT	TRANSMEM 305 325	POTENTIAL.	
FT	TRANSMEM 397 417	POTENTIAL.	
SEQUENCE	560 AA; 63247 MW; EAAA9CF15AA6AF49 CRC64;		

Db 4 GGEGLSLEFPTWVAVGCTVIVAISLAVLERLHYEGTVLKKKKOKPLXALQKKEELM 63
QY 66 LVGFISLLIVTQDPIIAKICISEDADVMPCKR----- 100
Db 64 LLGFISLLTVFQG-LISKFCVKENLHMMLPCSLDSRREAGASEHKNTAKEHQTFLP 122
QY 101 --GTEGRKPSKY---VDYCPK-GKVALMSTGSLHQLHVFIFVLAVFHVTSVITIALSR 153
Db 123 IVGTTTRLLAEHAAVQVGCSEKGVPLSLSEALHMLHIFVLALISHVFCVLTIVFGS 182
QY 154 LKMTWKKKMETETTSLEYQFANDP-----ARFRTHQTSFVKRH-LGLSTPGI-RMVV 205
Db 183 TRIHQKKWEDSIADKEF---DPETALRKRRVTHVNHAFIKEHFLGIGKDSVILGWTO 238
QY 206 AEFROFFRSVTKVDYLTLRAGFINAHLSONSKFDFHKYIKRSMEDDFKVVVGSILPLMGV 265
Db 239 SFLKQFYDSVTKSDYVTLRLGFIWTHCKGNPKLNHKYMMRALLEDDFKQVVGISWYLMIF 298
QY 266 ALLTFLLDINGVGTLLIWISIFIPVILLCVGTKLEMIEMALLEIODRASVIKAPVVEPS 325
Db 299 VVIFLLNVNGMHTYFWIAFIPALLAVGTLKLEHVIADLAHEVAEKHVAIEGDIYVKPS 358
QY 326 NKEFWHRPDWVLFIFHLTLFQNAFQMAHFVWTVAIPGLKCCYHTQIGLSIMKYVVGIAL 385
Db 359 DEHEWFSKQIVLYLIHILFQNAFEIAFEFWIMWTYGFDSICIMQOVRYIVPRLVIGVEI 418
QY 386 QFLCSYMTFPLLYALVTQMGSNMKSIFDEQTSKALTJNWRNTAKEKKKVRDITMLAQMIG 445
Db 419 QVLCSTPLPLXIVSOMGSSFKKAIFEENVOGLVGMACKYQKR-----DLKAAASNG 473
QY 446 DATPSR-GSSPMPSRGSSP 463
Db 474 DESSQAGPDPDSCSGSAP 492

RESULT 9
ML15_ARATH STANDARD; PRT; 496 AA.
ID ML15_ARATH O80580;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE MLO-like protein 15 (Atm1o15).
GN MLO15 OR AT2G44110 OR F6E13.24.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RT Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT "Molecular phylogeny and domain-specific co-evolution of the
RL plant-specific seven transmembrane MLO family.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT *Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana.";
RL Nature 402:761-768(1999).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -I- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC -----
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CC -----
CC EMBL; AF369576; AAK53808.1; -.
DR EMBL; AC004005; AAC23431.1; -.
DR InterPro; IPR004326; MLO.
DR Pfam; PF03094; MLO; 1.
KW Transmembrane; Multigene family.
FT TRANSMEM 10 POTENTIAL.
FT TRANSMEM 270 POTENTIAL.
FT TRANSMEM 398 POTENTIAL.
SQ SEQUENCE 496 AA; 56151 MW; 1B5FBE2DD33DFC3C CRC64;

Query Match 33.2%; Score 927; DB 1; Length 496;
Best Local Similarity 39.9%; Pred. No. 2e-70; Mismatches 168; Indels 52; Gaps 11;
Matches 205; Conservative 89; Mismatches 168; Indels 52; Gaps 11;

QY 12 LPETPSNAVAVVEAAMVLSVLMHGLHLKLGHWFOHRHKKALWEALEKMAEIMLVGIS 71
Db 8 LEYPTWVVALVCSVIVSISFAVELIHRAGKHFKNNDOKQLEGALQIKKEELMVGFS 67
QY 72 LLLIVTQDPIIAKICISEDADVMPCKRGTEGRKPSK-----YV 111
Db 68 LLLSVQSK-IAKICISKELSEKPLCTKPAGAEKSLSKDSHFQFSFTGRHLLAGDAPAG 126
QY 112 DYCP-EGKVALMSTGSLHQLHVFIVLAVFHTYSVTITIALSRKMTWKKEETTSLE 170
Db 127 DYCSLKGVPLMSLSALHELHIFIVLAVAHIIFFCLLTIVFGTWKIKQWKWKEDKY--LE 184
QY 171 YQFANDPARFRTH--QTSFVK-RHLGL-SSTPGIRWVVAFFROFFRSVTKVDYLTLRAG 226
Db 185 KDFDTQSIKRPHTVQEHFIRSRFLGVGAKADASLGWVQSEMKOFLASVNESDYITMLG 244
QY 227 FINAHLSONSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAILTLFLDINGVGTLLIWISFI 286
Db 245 FVTHCKTNPKFNFKYLMRALNSDFKVVGISWYLMVFVLLNLINIVAMHVEWLAFI 304
QY 287 PLVILLCVGTKLEMITMEMALLEIODRASVIKAPVVEPSNKFHWHRPDWVLFIFHLTLF 346
Db 305 PLILLAVGTLKEHITITDLAHEVAEKHVAIEGDLVVRPSDDLFWQSPRLVLIHILF 364
QY 347 QNAFQMAHFVWTVAIPGLKCCYHTQIGLSIMKYVVGIALQFLCSYMTFPLLYALVTOMGSN 406
Db 365 QNSEIAYFEFFILPQFGWDCIMDHVKFVYIPRLVIGVITQLLCSYSTPLPLXALVTOMGSS 424
QY 407 MKRSIFDEQTSKALTJNWRNTAKEKKKVRDITMLAQMIGDATPSRGSSPMPSRGSPVHL 466
Db 425 FKGAIFNEQTQEHLVGMAKMAKGVKKGATQVGTSH---DATSPRPSIQLNS-----L 474
QY 467 LHKGMGRSDDPQSAFPTSPRTQOEARDMYPVVVAH 500
Db 475 LKGGSSQONQ-----NPKKSE-----IAH 494

RESULT 10
YML3_ARATH STANDARD; PRT; 447 AA.
ID YML3_ARATH
AC 023693;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical MLO-like protein At1g11000.
GN AT1G11000 OR T19D16.26.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID-3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, Columbia;
RX MEDLINE-21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujit C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maliti R., Marziali A.,
RA Millscher J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
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or send an email to license@isb-sib.ch).
-----
DR EMBL: U95973; AAB65495.1; -.
DR InterPro: IPR004326; MLO.
KW Pfam: PF03094; MLO; 1.
KM Hypothetical protein; Transmembrane.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
SQ SEQUENCE 447 AA; 50608 MW; 027A1C33AE1B5EEA CRC64;
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Query Match 17.9%; Score 499.5; DB 1; Length 447;
Best Local Similarity 27.2%; Pred. No. 1.7e-34;
Matches 140; Conservative 72; Mismatches 159; Indels 143; Gaps 13;
OY 4 KKGVPARELPETPSWAVAVFAAMVLVSLMEHGLHKLGHWFOHRKKALWEALEKMAE 63
| : | | | | : | | : | | : | : | : | | |
DB 6 KEG--RSLAETPTYSVASVTVLVEFCFLVERAIRFRGXDY-GIHKVLLERTSS---- 57
OY 64 LMLVGFISSLIVTDPIIAKICISEDADAVMPCCKRGTEGRKPKSKYVDYCPEGKVALMS 123
| : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 58 -----TNQSSLPHHGIHEAS-----HQCGHGREFVS 84
OY 124 TGSLSQLHFVFENLAVEHVTVSVITIALSRCLKMRTWKKMETETSLEYGFANDPARFRFT 183
| | | | | : | | | | | : | : | : | : | : | : | : |
DB 85 YEGLEQLRFLEVLGITHTLVYSGIAGLAMSKL----- 117
OY 184 HGTSFVKRHIGLSSTPGIRWNVAAFFRQFRFSVTKVDTLLTRAGFINAHLSONSKFDFHKY 243
| | | | | : | | | | | : | : | : | : | : | : | : |
DB 118 -----CFLRQFRGISRKSDYFALRLGLTKH-NLPPTYNPFHM 154
OY 244 IKRSMEDDEKVVVGISLPLMGVAIIITLFELDINGVGTLLWISFIPLVILLGVGFKLEMIM 303
| : | | | : | | | | | : | : | : | : | : | : | : | : | : | : |
DB 155 MYRTMEDFEFGIVGISWPLMVYAIVCLINVHGLMNTFWISFVPAIIVLMVGTKLEHVS 214

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[illegible]


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Db      125 HFCLFONAFQLAFFIWSVYEFGIKTCFH 152
RESULT 12
ID       YHGE_ECOLI          STANDARD;          PRT;           574 AA.
AC       P45804;
DT       01-NOV-1995 (Rel. 32, Created)
DT       01-NOV-1995 (Rel. 32, Last sequence update)
DT       16-OCT-2001 (Rel. 40, Last annotation update)
DE       Hypothetical protein yhgE.
OS       YHGE OR B3402.
SN       Escherichia coli.
OC       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC       Escherichia.
OX       NCBI_TaxId=562;
RN       [1]
RP       SEQUENCE FROM N.A.
RC       STRAIN-K12 / MG1655;
RX       MEDLINE=97426617; PubMed=9278503;
RA       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA       Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA       Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA       Mau B., Shao Y.;
RT       "The complete genome sequence of Escherichia coli K-12.";
RL       Science 277:1453-1474(1997).
CC       -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC       -1- SIMILARITY: SOME, TO B.SUBTILIS YRDB.
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-----
DR       EMBL; U18997; AAA58199.1; -.
DR       EMBL; AE000415; AAC76427.1; -.
DR       EcoGene; EG12931; yhgE.
KW       Hypothetical protein; Transmembrane; Complete proteome.
FT       TRANSMEM     12      32      POTENTIAL.
FT       TRANSMEM     39      59      POTENTIAL.
FT       TRANSMEM     66      86      POTENTIAL.
FT       TRANSMEM     99     119      POTENTIAL.
FT       TRANSMEM    142     162      POTENTIAL.
FT       TRANSMEM    178     198      POTENTIAL.
FT       TRANSMEM    214     234      POTENTIAL.
FT       TRANSMEM    248     268      POTENTIAL.
FT       TRANSMEM    286     306      POTENTIAL.
FT       TRANSMEM    320     340      POTENTIAL.
FT       TRANSMEM    353     373      POTENTIAL.
SQ       SEQUENCE      574 AA;      64637 MW;      529EB33C38D5BEF59 CRC64;
Query Match              3.7%; Score 102.5; DB 1; Length 574;
Best local Similarity   19.7%; Pred. No. 0.61;
Matches 69; Conservative 53; Mismatches 89; Indels 139; Gaps 16;

Oy      111 VDYPEGVAALMSTGSLHQHLVFIFVL-----AVFHV-----TYSVIT--- 148
        | : | : ::||| | | : : :         | : | :         :||| :
Db      4 VELSPATRMGMATGLGGLVCYLIIAIVLSGKNHSWIVYGVPATVAFSSVLLFSVISFKQ 63
Oy      149 -----IALSRLKMRTWKKWTETETS-----LEEQ 172
        : : : | | | ||| : :
Db      64 KRLMGWLALVFATPLGMSGWLKWQTGDMPRAEKALWDFGCYLLIMAMLLPWIQQSLR 123
Oy      173 FANDPARFRPTHQTSF--VKRHGLGSTPGIRWVV-----APPRQFFRSVTK 217
        || :||| : :| : | : | : | : | : | : | : | : | :
Db      124 IRNDSRYRYFYQSVMHNVLILLVIFLANGLTWLVLLMWSELFKLVGITFEENTLFPATDW 183
Oy      218 VDYLTLRAGFINA-----HLSQNSKFDFHKYIKRSMEDDFKVVGIGISLPWGVAILLTLFL 272
        ||||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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Db      184 FIVLTL--GLVTALAVILARTQSRLID-----SIÖKFLTLIATGLLPL--VSLLTLMF 232
QY      273 -----DINGVGTLLWISFIPVLILCVGTKLEMIMEMALEIQDRAS----- 314
Db      233 ITLTPGTLSAISRHISAAGLLLTFLA-----LÖLILMAIVRDPÖ--KASLPWT 279
QY      315 -----VIKGAPEVPEPSNKEFWFHRPDWVLFPIHTLTLFÖNAFÖMAHFVMTV 359
Db      280 GPLRLIKLTALIVAPLVYFV---AAWALW-----LRVAÖYGWTV 315

RESULT 13
HSLU_HELPJ ID HSLU_HELPJ STANDARD; PRT; 443 AA.
AC Q9ZLW1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE ATP-dependent hsl protease ATP-binding subunit hslU.
GN HSLU OR JHP0465.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummaho P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
CC COMPLEX (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
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CC -----
CC EMBL; AE001480; AAD06034.1; -
CC HSSP; P32168; IDO2.
CC InterPro; IPR003593; AAA.
CC InterPro; IPR003959; AAA_subfam.
CC InterPro; IPR001270; CLP_AB.
CC Pfam; PF00004; AAA; 1.
CC PRINTS; PR00300; CLP_PROTEASEA.
CC SMART; SM00382; AAA; 1.
CC Chapterone; ATP-binding; Complete proteome.
FT NP_BIND 59 66 ATP (POTENTIAL).
FT SEQUENCE 443 AA; 50164 MW; 6AF0F90849B686DA CRC64;

Query Match 3.4%; Score 95.5; DB 1; Length 443;
Best Local Similarity 22.2%; Pred. No. 1.7;
Matches 54; Conservative 35; Mismatches 95; Indels 59; Gaps 12;

QY 34 MEGHLHKGHWFOHRRKKAL--WEALEKKAEL--MLVGFI-----SLLIVT 77
Db 196 VQENLIKVFHKEQDKVKKTLISVKEAKALKAELISDTLLDGEAIKMEGLKRAESSGVIFID 255
QY 78 QDPIARIKICISEDADVMWPCRGTEGRKPSKYVDYCP--EGKVALMSTGSLHQLHVFIF 135
Db 256 E--IDKIAVSSKEGSRQDPFSKEGVÖR-----DLLPIVEGSVNTKYGSIKTEHILFI 305

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QY 136 VLAVFHT--YSVITIALSRKMKETETTSLEYQFANDPARFRTHTQSFVKRHL 193
DB 306 AAGAFHLSKPSDLPELOGRFLRV--ELENLTEEMIMLTQT-----KTSIIKQYQ 356
QY 194 GLSTPGIRWVAFERQFRSVTKVDYLLRAGFINAHLSONSKFD-----FKYIKRS 247
DB 357 ALLKVEGE--IAFEDDAIKELAKLSY-----NANQKSEDIGARLHTTIKV 402
QY 248 MED 250
DB 403 LED 405

RESULT 14
NFIC_PIG STANDARD; PRT; 506 AA.
AC P21999;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nuclear factor 1 C-type (Nuclear factor 1/C) (NFI-C) (NFI-C) (NFI-C)
DE (CCAAT-box binding transcription factor) (CTF) (TGGCA-binding protein).
GN NFIC OR NFI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90105327; PubMed=2513876;
RA Meisterernst M., Rogge L., Foeckler R., Karaghiosoff M., Winnacker E.L.;
RT "Structural and functional organization of a porcine gene coding for nuclear factor 1."
RL Biochemistry 28:8191-8200(1989).
CC -1- FUNCTION: RECOGNIZES AND BINDS THE PALINDROMIC SEQUENCE 5'-TTGGCANNNGCCAA-3' PRESENT IN VIRAL AND CELLULAR PROMOTERS AND IN THE ORIGIN OF REPLICATION OF ADENOVIRUS TYPE 2. THESE PROTEINS ARE INDIVIDUALLY CAPABLE OF ACTIVATING TRANSCRIPTION AND REPLICATION.
CC -1- SUBUNIT: BINDS DNA AS AN HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE CTF/NFI FAMILY.
CC -1- SIMILARITY: CONTAINS 1 DNA/MHI DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02875; AAA31093.1; .
DR PIR: A33416; A33416.
DR TRANSEFAC; T00175; .
DR TRANSEFAC; T00538; .
DR InterPro; IPR000647; CTF_NFI.
DR InterPro; IPR003619; Dwarfin_A.
DR Pfam; PF00859; CTF_NFI; 1.
DR SMART; SM00523; DMA; 1.
DR PROSITE; PS00349; CTF_NFI; 1.
KW Transcription regulation; DNA replication; DNA-binding; Activator; Nuclear protein; Multigene family; Alternative splicing.
FT DOMAIN 68 176 DMA.
SQ SEQUENCE 506 AA; 55461 MW; 6315A9474807F4C0 CRC64;

Query Match 3.4%; Score 95.5; DB 1; Length 506;
Best Local Similarity 23.7%; Pred. No. 2;

Matches 66; Conservative 38; Mismatches 102; Indels 73; Gaps 15;
QY 291 LLCV-----GKLEIMEMALEIODRASVIKAPVPEPSKFEWHRPDWLFETHLTL 345
DB 161 VLCVQPHHIGVAVKELDYLAIFYVERDAEQSGSPRAGMG-----DOEDSKPITLDTTD 215
QY 346 FQNAFQMAHFVWVATPGLKKCYHTQIGLSIMKVVGIALQF---LCSYMTFPLVALVT 401
DB 216 FOESF-VTSGVFSVT-----ELIQVSRTPVVTGTGPNFSLGELQGMAYDLNPAST 265
QY 402 QM-----GSMKRS-----IFDEQTSKALTNWNTAKE-----KKK 432
DB 266 GMRRTLPTSSSGSKRHKSGSMEEDVDTPGGDYTSPPSSPTSSN-RNWTEDMEGIGSSP 324
QY 433 VRDMDLMAQMTGDATPSRGSSPMPS-RGSS-----PVHLHKMGSRSDDPQSA---PT 482
DB 325 VKKTEM-----DKSPFNSSPQDSDPRLSSFTQHHRPVIAVHSGIARSPHSSALHPPT 377
QY 483 SPRTQGEARDMYP-VVVAHPVHRLNPDRRRSASSALE 520
DB 378 TSILPQTASTYFPHTAIRYPH-LNPQDPLKDLVSLACD 415

RESULT 15
YD49_THEME
ID YD49_THEME STANDARD; PRT; 338 AA.
AC 09X170;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TM1349.
GN TM1349.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima."
RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001789; AAD36420.1; .
DR TIGR; TM1349; .
DR InterPro; IPR002549; UPF0118.
DR Pfam; PF01594; UPF0118; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 203 223 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
SQ SEQUENCE 338 AA; 39386 MW; 9B21A19682078ADD CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2002, 13:30:27 ; Search time 24.92 Seconds
(without alignments)
522.425 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSMAV.....ASSALADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2788	100.0	533	4	US-09-350-268-3	Sequence 3, Appli
2	1257	45.1	515	4	US-09-183-959-10	Sequence 10, Appl
3	888.5	31.9	492	4	US-09-183-959-2	Sequence 2, Appli
4	801.5	28.7	496	4	US-09-350-268-2	Sequence 2, Appli
5	752.5	27.0	264	4	US-09-183-959-12	Sequence 12, Appl
6	730.5	26.2	509	4	US-09-183-959-8	Sequence 8, Appli
7	478	17.1	114	4	US-09-183-959-14	Sequence 14, Appl
8	193	6.9	80	4	US-09-183-959-4	Sequence 4, Appli
9	129	4.6	52	4	US-09-183-959-6	Sequence 6, Appli
10	93.5	3.4	339	4	US-09-323-873A-2	Sequence 2, Appli
11	90.5	3.2	2787	4	US-09-245-041-15	Sequence 15, Appl
12	89.5	3.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
13	88	3.2	652	1	US-08-050-684-2	Sequence 2, Appli
14	88	3.2	652	1	US-08-582-719-2	Sequence 5, Appli
15	87	3.1	1835	4	US-09-404-650-5	Sequence 10, Appl
16	85	3.0	364	2	US-08-458-970A-10	Sequence 20, Appl
17	85	3.0	630	4	US-09-300-909-20	Sequence 70, Appl
18	82.5	3.0	765	4	US-08-444-818-70	Sequence 42, Appl
19	81.5	2.9	773	2	US-08-484-101B-42	Sequence 44, Appl
20	81.5	2.9	773	2	US-08-484-101B-44	Sequence 42, Appl
21	81.5	2.9	773	4	US-08-714-524D-42	Sequence 44, Appl
22	81.5	2.9	773	4	US-08-843-417-2	Sequence 2, Appli
23	80	2.9	1956	4	US-09-331-581-2	Sequence 2, Appli
24	78	2.8	581	4	US-08-788-231A-2	Sequence 12, Appl
25	77.5	2.8	465	3	US-08-928-692-12	Sequence 2, Appli
26	77.5	2.8	524	2	US-09-404-650-2	Sequence 2, Appli
27	77	2.8	2175	4		

28	77	2.8	2188	4	US-09-404-650-4	Sequence 4, Appli
29	76.5	2.7	350	1	US-08-118-270-41	Sequence 41, Appl
30	76.5	2.7	350	5	PCT-US93-08528-41	Sequence 41, Appl
31	76.5	2.7	473	1	US-08-439-131A-4	Sequence 4, Appli
32	76.5	2.7	473	1	US-08-440-674-3	Sequence 3, Appli
33	76.5	2.7	663	4	US-08-959-004-5	Sequence 5, Appli
34	76.5	2.7	1440	4	US-09-357-251-37	Sequence 37, Appl
35	76	2.7	318	1	US-08-309-182B-3	Sequence 3, Appli
36	75.5	2.7	782	4	US-08-669-286-10	Sequence 10, Appl
37	75.5	2.7	782	4	US-09-469-253-10	Sequence 10, Appl
38	75.5	2.7	782	4	US-09-642-146-10	Sequence 50, Appl
39	75.5	2.7	2353	4	US-08-984-709A-50	Sequence 3, Appli
40	75	2.7	407	2	US-08-742-440A-3	Sequence 2, Appli
41	75	2.7	430	1	US-08-601-435-2	Sequence 2, Appli
42	75	2.7	430	2	US-08-931-047-2	Sequence 2, Appli
43	75	2.7	430	2	US-08-783-202-2	Sequence 2, Appli
44	75	2.7	601	2	US-08-795-868-16	Sequence 16, Appl
45	75	2.7	602	4	US-09-303-069-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-350-268-3
; Sequence 3, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
; FILE REFERENCE: 5718-42A-- M103
; CURRENT APPLICATION NUMBER: US/09/350, 268
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-09-350-268-3

Query Match	100.0%;	Score 2788;	DB 4;	Length 533;											
Best Local Similarity	100.0%;	Pred. No. 2.9e-294;													
Matches 533;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;											
QY	1	MSDKKGVPA	RELPE	TPSNAAVFA	AMVLSVLM	HGLHKLGH	WFQHRH	KKALWE	LEKM	60					
DB	1	MSDKKGVPA	RELPE	TPSNAAVFA	AMVLSVLM	HGLHKLGH	WFQHRH	KKALWE	LEKM	60					
QY	61	KAEMLDVGF	ISLLIVTQ	DPPIAKIC	ISEDAD	VMWPC	KRGTEGR	PKSKYV	DYCE	PGKVA	120				
DB	61	KAEMLDVGF	ISLLIVTQ	DPPIAKIC	ISEDAD	VMWPC	KRGTEGR	PKSKYV	DYCE	PGKVA	120				
QY	121	LMSTGSLHQL	HVFIFVLAV	FHVYYSV	ITIALSR	LKMRTW	KKWETET	SLEYOF	ANDPAR	F	180				
DB	121	LMSTGSLHQL	HVFIFVLAV	FHVYYSV	ITIALSR	LKMRTW	KKWETET	SLEYOF	ANDPAR	F	180				
QY	181	RFTHTSFWK	RHLGLS	STPGIR	WVAFF	RFQFF	RSVT	KVDY	TLRAG	FINAHL	SQNSK	FD	240		
DB	181	RFTHTSFWK	RHLGLS	STPGIR	WVAFF	RFQFF	RSVT	KVDY	TLRAG	FINAHL	SQNSK	FD	240		
QY	241	HKYIKRSM	EDDFK	VVVGIS	LPLMG	VALTL	FLDING	VGTL	LIWIS	FIP	VLILL	CVG	T	LEM	300
DB	241	HKYIKRSM	EDDFK	VVVGIS	LPLMG	VALTL	FLDING	VGTL	LIWIS	FIP	VLILL	CVG	T	LEM	300
QY	301	IIMEMALE	IQDRAS	VIKGAP	VVEPS	NKFFW	HRPD	WVLF	FIHL	TLFQ	NAFQ	MAHF	W	TVA	360
DB	301	IIMEMALE	IQDRAS	VIKGAP	VVEPS	NKFFW	HRPD	WVLF	FIHL	TLFQ	NAFQ	MAHF	W	TVA	360
QY	361	TPGLKCYH	TQIGLS	IMKVV	VGIALO	FLCSY	MTFPL	YALV	TQMG	SNNK	RSIF	DEOT	S	KAL	420
DB	361	TPGLKCYH	TQIGLS	IMKVV	VGIALO	FLCSY	MTFPL	YALV	TQMG	SNNK	RSIF	DEOT	S	KAL	420

Db 361 TPGLKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTQMGSNMKSIFDEQTSKAL 420
QY 421 TNRNRTAKEKKKVVDTMDLMAQMGIDATPSRGSSPMPSRGSSPVHLHKMGSRDDPOSA 480
Db 421 TNRNRTAKEKKKVVDTMDLMAQMGIDATPSRGSSPMPSRGSSPVHLHKMGSRDDPOSA 480
QY 481 PTSPRTQGEARMDYPPVVAHPVHRNPNDRRRSASSALSADIPSADFSF50G 533
Db 481 PTSPRTQGEARMDYPPVVAHPVHRNPNDRRRSASSALSADIPSADFSF50G 533

RESULT 2
US-09-183-959-10
; Sequence 10, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 10
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-10

Query Match 45.1%; Score 1257; DB 4; Length 515;
Best Local Similarity 48.7%; Pred. No. 7.3e-128;
Matches 251; Conservative 84; Mismatches 116; Indels 64; Gaps 7;

QY 6 GVPARELPETPSWAVAVFAAMVLYSVLMEHGLHKLGHWFQHRHKKALWEALEKKAEIM 65
Db 7 GGNRELDQPTMAVAVSCVGVITLLEKGLHVGFEFSHRKKKAMEALEKKAEIM 66
QY 66 LVGFISILLVYODPIIAKICISEDADVMWPK-----RGTE----- 103
Db 67 VLGFISILLVFGQNYII-KVCISNHNANTMLPCKLEAAVEGKDGHEKAAYVAGKKV 125
QY 104 -----GRKPSK-----YVDY-----CPEGKVALMSTGSLH 128
Db 126 AVAVPGKKKKKAAADHDLGVVDWMPREYYAHNARMLEASMAKCPREGKVALMSTGSLH 185
QY 129 QLHVFIFVLAVFHTYVTITIALSRKMTWKMETETTSLEYQFANDPARFRTHQTSF 188
Db 186 QLHVFIFVLAVFHTYVTITIALSRKMTWKMETETTSLEYQFANDPARFRTHQTSF 188
QY 189 VKRHLG-LSTPGIRWVVAFFRQFRSVTKVDYLTLRAGFTNAHLSQNSKFEHFKYKRS 247
Db 246 VRQHMNVLNKFPASFYISNFRQFRSVTKVDYLTLRAGFTNAHLSQNSKFEHFKYKRS 305
QY 248 MEDDFKVVVGLISLPLMGVAITLFLDINGVGTLLWISFIPVILLCVGTKLEMIMEMAL 307
Db 306 LEDDFKVVVGLISLPLMGVAITLFLDINGVGTLLWISFIPVILLCVGTKLEMIMEMAL 365
QY 308 EIODRASVIKGAPEVPSNKFVWHRPDLVLFILTLFQNAFQMAHFWVTATPGLKCC 367
Db 366 DITERHAVIOGIPWVQVSDSYFWFAPRTFVLFILTLFQNAFQMAHFWVTATPGLKCC 425
QY 368 YHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTQMGSNMKSIFDEQTSKALTNMNTA 427
Db 426 FNDSEEFVFAFLCLGVVVOVLCSYVTLPLVALVSQMGSTMKOSIFDEQTSKALKNMNTA 485
QY 428 KEKKKVRDTMDLMAQMGIDATPSRGSSPMPSRGSS 462

Db 486 KKKAPTTG-----SKHGGGSPTAGGSPTKADGDA 515

RESULT 3
US-09-183-959-2
; Sequence 2, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-2

Query Match 31.9%; Score 888.5; DB 4; Length 492;
Best Local Similarity 38.9%; Pred. No. 7.7e-88;
Matches 187; Conservative 96; Mismatches 157; Indels 41; Gaps 8;

QY 9 ARELPETPSWAVAVFAAMVLYSVLMEHGLHKLGHWFQHRHKKALWEALEKKAEIMLVG 68
Db 7 AALEFTPTWIVAACSLIVLSTVAERCLHYLGKTLKRKNQKPLFEALIKVEIMLLG 66
QY 69 FISLLIVTODPIIAKICISEDADVMWPKR-----GTEGR-----K 106
Db 67 FISLLIVTODPIIAKICISEDADVMWPKR-----GTEGR-----K 106
QY 107 PSKYVDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHTYVTITIALSRKMTWKMETE 165
Db 126 GTAGAEOCKKKVLDLSLAIHQHIFVLAITHVIFSVTMLLGAQIHOWQWE-- 183
QY 166 TTSLEYQFANDPARFRTHQTSFVKRH---LGLSTPGIRWVVAFFRQFRSVTKVDYLT 222
Db 184 NGIKKDPAGNGPKVTNVHHEFIKKRREKIGKDSII-LSWLSHSGKOFYRSVSKSDYTT 241
QY 223 LRAGFINAHLSONSKFEHFKYKRSMEDEKVVVGLISLPLMGVAITLFLDINGVGTLLW 282
Db 242 MHLGFIHTHCPNRPDEHRYMVRVLEADFKKVVGISWYLMVFWVIFLLNVNGWHTYFW 301
QY 283 ISFIPVILLCVGTRKLEMIMEMALEIODRASVIKGAPEVPSNKFVWHRPDLVLFILH 342
Db 302 IAFPLILLAIIGTRLEHVIQAOLAHVDAEKHTAVEGDVIVKPSDEHFWGKPRVILYLH 361
QY 343 LTLFQNAFQMAHFWVTATPGLKCCYHTQIGLSIMKVVVGLALQFLCSYMTFPLVALVTO 402
Db 362 FILFQNAFEIAFFFWLSTYGFDSKMGVRFIVPRVIGVYIQLCSYSTPLVALVTO 421
QY 403 MGSNMKSIFDEQTSKALTNMNTAKEKKKVVDTMDLMAQMGIDATPSRGSSPMPSRGSS 462
Db 422 MGSNCYKKEIFNEHVQGVLGWAQVKMKKGLK-----GAASAKDESTINADSAG 471
QY 463 P 463
Db 472 P 472

RESULT 4
US-09-350-268-2
; Sequence 2, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:


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OY 160 KKWEETTSLEYOFANDPARFRFT----HOTSFYKRLHG--LSSTPGIRWVAVFRQEFFR 213
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Db 173 RKWET---LAGPIAAEELKARRTKVMRRQSTFVFNNAHPWSKNKILIMLCFLRQFKG 228
OY 214 SVTKVDYLTLRAGFINAHLSONSKFDFHKYIKRSMDEDFKVVVGISLPLMGVAIITLFLD 273
| : : | | | | | : | : | | | | | : | | | | | : | : | : : |
Db 229 SIIRSDYLALRLGFWYHKLPHS-YDFHKYVMRSMEDDYNGTIGISWPLMAYAIVCILIN 287
OY 274 INGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFWEHR 333
:| : : | : : : : | | | : : | : | : : | : : : : | : : |
Db 288 VHGINIYFWLSFVPVILVLTGTELQHVIAQLALEVAEATAFYVGSQ-LKLRDLEWFGK 346
OY 334 PDWVLFPIHILTFQNAFQMAHFVWTVATPGLKKCYHFOIGLSIMKVVGALQFLCSYMT 393
| : : | | | | | : | : | : : | : : : : | : : | | | |
Db 347 PRYLWMLIOFISFQNAFELATFLMSLWELSAQTCFMRKHYMVAIRLISGLLVQFMCYST 406
OY 394 FPLVALVTOMGSNMKRSIFDEQTSKALTNRNTAKEKKK 432
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Db 407 LPLNVIISQMGPKFKKSLVSENVRESLHSWCCKRVKDRSR 445
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RESULT 7
US-09-183-959-14
; Sequence 14, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-183-959-14
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Query Match 17.1%; Score 478; DB 4; Length 114;
Best Local Similarity 74.6%; Pred. No. 3.2e-44;
Matches 85; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
OY 322 VEPSNKFWEHHRPDVLFHILTLFQNAFQMAHFVWTVATPGLKKCYHFOIGLSIMKVAV 381
||||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 VEPSDRFWEHNRGFWLFIHILTLFQNAFQMAHFVWTLITPDLKKCYHERLGLSIMKVAV 60
OY 382 GLALQFLCSYMTFPLVALVTOMGSNMKRSIFDEQTSKALTNRNTAKEKKKVRD 435
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GLVLQVLCSYITFPLVALVTOMGSNMKRTIFEQTAKAVMKRRKTAKDVRORE 114
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RESULT 8
US-09-183-959-4
; Sequence 4, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
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; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 4
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-183-959-4
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Query Match 6.9%; Score 193; DB 4; Length 80;
Best Local Similarity 51.3%; Pred. No. 1.8e-13;
Matches 40; Conservative 11; Mismatches 27; Indels 0; Gaps 0;
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OY 231 HLSQNSKDFHFKYIKRSMDEDFKVVVGISLPLMGVAIITLFLDINGVGTLIWISFIPVI 290
| : : | | | | | : | : | | | | | | | | | | | | | : : | : |
Db 1 HPEKPDIDFHKYMTRAVEYEFKRVVGISWVLMFLVILFLLNLINGWHTFYWLAFLPLFL 60
OY 291 LILCVGTKLEMIIMEMALE 308
| | | | | | | | | | | | | | | | | |
Db 61 LLIVGAKLEHITITRLAE 78
```

```
RESULT 9
US-09-183-959-6
; Sequence 6, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
; US-09-183-959-6
```

```
Query Match 4.6%; Score 129; DB 4; Length 52;
Best Local Similarity 46.2%; Pred. No. 8.1e-07;
Matches 24; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
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```
OY 383 LALQFLCSYMTFPLVALVTOMGSNMKRSIFDEQTSKALTNRNTAKEKKKVR 434
: : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 VVIXLCSYSTPLPLAIVTOMGSCYKKEIFNEHVQGVLGWAQVKMKKGLR 52
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```
RESULT 10
US-09-323-873A-2
; Sequence 2, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
```

```

; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-323-873A-2

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Query Match	3.4%;	Score 93.5;	DB 4;	Length 339;
Best Local Similarity	21.7%;	Pred. No. 0.11;		
Matches	68;	Conservative	48;	Mismatches 113;
				Indels 85;
				Gaps 16;

QY	2	SDKKGVPARELPET---	PSW----	AVAVFEAMVLVSVMHEGLHKIGHWFQHRHKKAL	53
Dd	52	ADEFDPCS-ELQHTQELFPQWHLPRIKAIAIASLTFELYTLREVIHPLATSHQQYFYKIP			110
QY	54	WEALEKMAEIMLVGFISSLIVTQDEPIAKICISEDADAVMWPCKRGTEGRKPSKYVDY			113
Dd	111	ILVINKV---LPMVS-ITLLALVYLPBGVLAIV-----	QLHGNTKYRKPPEPHLD-		155
QY	114	CPEGKVALMSTGSLHQHVFEIFVLAVEFHYTVSVITIALS-----	RUKMRTRWKMETET		166
Dd	156	----KWML-----TRKQGILLSFFFAVLHAHYS-----	LSPMRRSRYRKLLNWAYQQVVOQ		202
QY	167	TSELYOEPANDPARFRFTHQTSFV----	KRHJLSSTPGI----	RWVVAEFFROQERSVTKV	218
Dd	203	NKEDANIEDHWARMETIYVSLGTVGAIALLAVALTSIPSVSDSLTV-----	REFHYIQSKL		257
QY	219	DYLTLRAGFTNAHLSONSKFDPFKYIKRSMEDDEFVVVGISLPLMGVAIIITLFLDINGVG			278
Dd	258	GIVSLLGTITHALI-----FAMNKWI-----	DIKQFWYTPTPFMIAY-----		295
QY	279	TLIWISFTPLVILL	292		
Dd	296	-----FLPIVILI	303		

```

RESULT 11
US-09-245-041-15
; Sequence 15, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: MOORE, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 2787
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-041-15

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Query Match	3.2%;	Score 90.5;	DB 4;	Length 2787;
Best Local Similarity	18.5%;	Pred. No. 6.7;		
Matches	89;	Conservative	64;	Mismatches 190;
				Indels 137;
				Gaps 20;

QY	85	ICISEDADVWMPCKRGTEGRKPSKYVDYCPEGKVALLMSTGSLHQLHVFEVLAVENHTY	144
Dd	1447	ICREGRGEMAVRC--GTEDMKP SKHLTHLHDKLSL---TVSPIRVPASNLLILHRKY	1500
QY	145	SVITI-----ALSRLKMRTWKMETETTSLEYQFANDPARFRFTHQTSFYVKRHLGL	195
Dd	1501	LILVOGADGCWRRPVSQENEHSGLMKTVLGVSTVQTKDKDGVFTSRHSSSVYLEH-GL	1559
QY	196	SSTPGIRWVAVFROFERSVTKVDYLTLRAGFINAHLSONSKFDFHKYIKRSMEDDEKVV	255
Dd	1560	LKTSQMLNLFISLSFLKDVL-----FILARFQLSLFO-----	1593
QY	256	VGISLPL--WGVALITLEDINGV-----GTLIWISFIPLVILLCVGKLEMI	301
Dd	1594	-GVPFVLVENWSISFDHIKLKGXGYFKQGQQCYFECKLVVEYSNLINLYLIHLKLSL-	1651
QY	302	IMEMALLEIODRASVIKGA VYEPSPNKFFWFHPRPDWLFEFHLLTFONAFOMAHFWTVAAT	361
Dd	1652	-----PESLP-----VPLLHLTL-----PLSHI-----	1670
QY	362	PGLKKCYHTOIGLSIMKVVGJLAOLFCSYMTFPLVALY---TOMGSNMKRSI FDEQTSK	418
Dd	1671	-----HTQTHNTK-CLDEPKIQLESADVFTLHSLYLVKEKLP LAICFESKIF--AARK	1720
QY	419	ALTNRN--TAKEKKKVRDTMLMAQMIGDATPSRGSSPM-----SRGSSPVHLL	467
Dd	1721	EFSHPRNIISSRDERKAEMNELKLLFLSKRTISR-RRPLPPCHPRDPDKRSEERTHSC	1779
QY	468	HKGMSDD-----POSAPTSPTQOEARDMPVVVAHVPHRLNPNDRRRSASSSAALEA	521
Dd	1780	HASLSREHEHLGPLDORASVCPAASSE-----LVVHGQGVDS DAKRG TASHCQA EA	1832

```

RESULT 12
PCT-US94-00198-4
; Sequence 4, Application PC/TUS9400198
; GENERAL INFORMATION:
; APPLICANT: Schering Corp.
; TITLE OF INVENTION: RAS Associated GAP Proteins
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering Corp.
; STREET: 1 Girard Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 94304-1104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 6.0.8
; SOFTWARE: Microsoft Word 5.1a
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00198
; FILING DATE:
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/004,824
; FILING DATE: 15-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: DX0352 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)822-7255
; TELEFAX: (201)822-7039
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3079 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
PCT-US94-00198-4

Query Match 3.2%; Score 89.5; DB 5; Length 3079;
Best Local Similarity 18.6%; Pred. No. 10;
Matches 95; Conservative 73; Mismatches 165; Indels 179; Gaps 22;

OY 90 DADVMPCRKRTGKRPSTKYVD-YCEPKV-----ALMSTGSLHQ----- 129
DB 1190 DSEKLTPLIMGTGR--ALFVSLYSSQKIEKTLKIAYTEYLSAINFHERNIDADKTW 1247
OY 130 LHVFIPLVAVHVTYSVT-TIALSR-----LKMRT-----WKKEETET--T 167
DB 1248 VHNIEFVEAMCHDNYTSGSIAFQRTTRNNILRFATIPNAILLDSMRMITYKKWHTYTHSK 1307
OY 168 SLEYOAFANDPARFRTHQTSFVKRHLGLSTPGIRWV-VAEFRQFRSVTKVDYTLRAG 226
DB 1308 SLEKQERNDFRNAGI-----LASLSGILFINKKILQEMYPYL-LDTVSELKK 1354
OY 227 FINAHLSONSKF-DFHKYIKRSMEDDFKVVV-----GISLPLMGVAITLFLDI 274
DB 1355 NIDSFISKOCQWLNYPDLTFRNSRDILSVELHPLSFNLFNNLRKLKELACSDLSIPE 1414
OY 275 NGVGTLLWISFIPVLILCVGKLEMIIMEMALEIODRASV-----IKGAPVVEPSNKF 330
DB 1415 NESSVYLLEQIIMKRLTILGRDDNYVMMLFSTEIVDLIDLTLDEIKKIPA----- 1465
OY 331 FHRDQVLFIFHILTLFQNAFQMAHFVWTATPGLKKCYHFGIGLSIMKVVGALQFLCS 390
DB 1466 -YCPKYLKAITQMTKMSALOHSE-----VNLGVKNHFHVK----- 1500
OY 391 YMTFPLVALVTQMSNMKRSIFEDQTSKALTNW-----RNTAKEKKV---RD 435
DB 1501 -----NKWLKQITDWFQVSIAREYDENLSKPLKEMDLVKRD 1537
OY 436 TDMTMAQMGIDAT-----PSRGSSPMPSRGSSPV-----HLHKMGGRSD 476
DB 1538 MDLYIDTAIEASTAIAYLTRHTFLEIPPAASDPELSRSRSVIFGFYFNILMKGLEKSSD 1597
OY 477 PQSAPTSPTQOEARMYPVVVAHPVHRLNPN 508
DB 1598 -----RDNYPVFLRHKMSVLYNDN 1615

RESULT 13

US-08-050-684-2
Sequence 2, Application US/08050684
Patent No. 5550221
GENERAL INFORMATION:
APPLICANT: Johann Dr., Stephen V.
APPLICANT: Van Zeijl Dr., Marja
APPLICANT: O'Hara Dr., Bryan M.
TITLE OF INVENTION: Amphotropic Virus Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street
CITY: Stamford
STATE: CT
COUNTRY: United States of America
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,684
FILING DATE: 16-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Lowney Dr., Karen A
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 31937-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-684-2

Query Match 3.2%; Score 88; DB 1; Length 652;
Best Local Similarity 19.4%; Pred. No. 1.3;
Matches 78; Conservative 41; Mismatches 120; Indels 164; Gaps 16;

OY 222 TLRAEFINAHLSONSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAITLFLDING----Y 277
DB 69 TIRKGIIDVNL-----YNETVETLMAGEVSAMVGA--VWOLIASFLRLPISGTHCIV 119
OY 278 GTLLWISFIPVLILCVGK---LEMI-----IMEMALEIODRASVYK-- 317
DB 120 GSTIGFS-----LVAIGTKGVQMMELVKIVASWFISSLGFSMGLLFVLIRIFILKE 173
OY 318 -----GAPVVEPSNKFVFWHPRDQVLFHILTLFQNA 349
DB 174 DVPVNGLRALPVFYAATIAINVESIMYTGAPVL-----GLVLPMA--TALISFGVA 223
OY 350 FQMAHFVWTATPGLKKCYHTQIGLSIMKVVGALQFLCSYMTFPLVALVTQMSNMK 409
DB 224 LLEAFVWL-----FVCPWMRKRTGKLOKGAISR- 254
OY 410 STFDEQTSKALTNRNTAKEKKVBDTDLMAQMGIDATPSRGSSPMPSRGSSP----- 463
DB 255 -VSDESLSKVQEAESPVEKELPGAKANDDSTIPLTGAAGETLGTSEGTSAESHPRAYGR 313
OY 464 -----VHLHKMGGRSD-----PQSAPTS 483
DB 314 ALSMTHGSVKSPISTNGTFGFDGTRSDGHVYHTVHKDSGLYKDLLKIHIDRGPEEKPAQ 373
OY 484 PRTQGEAR--DMYPVVVAH---PVHRLNPNDRRSSASSALE 520
DB 374 ESNYRLLRNNSYCYTAICGLPVHA-----TFRAADSSAPE 411

RESULT 14

US-08-582-719-2
Sequence 2, Application US/08582719
Patent No. 5633348
GENERAL INFORMATION:
APPLICANT: Johann Dr., Stephen V.
APPLICANT: Van Zeijl Dr., Marja
APPLICANT: O'Hara Dr., Bryan M.
TITLE OF INVENTION: Amphotropic Virus Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street
CITY: Stamford
STATE: CT
COUNTRY: United States of America
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,719

FILING DATE: 04-JAN-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,684
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 31937-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-582-719-2

Query Match 3.2%; Score 88; DB 1; Length 652;
Best Local Similarity 19.4%; Pred. No. 1.3;
Matches 78; Conservative 41; Mismatches 120; Indels 164; Gaps 16;

QY 222 TLKAGFINAHLSONSKFDFHKKYIKRSMEDDFKVVVIGISLPLMGVAITLFLDING----V 277
DB 69 TIRKGIIDVNL-----YNETVETLMAGEVSAMVGS--VWQLIASFLRLDISGTHCIV 119
QY 278 GTLIWISFIPVLICVGTGK---LEMI-----IMEMALEIODRASVIK-- 317
DB 120 GSTIGFS-----LVAIGTKGVQWMLVKIVASMFISPLLSGFMGSLFVLRIFILKE 173
QY 318 -----GAPVVEPSNKFVWFHPRDPWVLFTHLLFQNA 349
DB 174 DVPVNGLRALPVFYAATIAINVSIMYTGAPVL-----GLVLPMA--IALISFGVA 223
QY 350 FQMAHFVWTVAATPGKCKYHTQIGLSIMKVVVGLALQFLCSYMTFPLIYALYTOMGSNMKR 409
DB 224 LLFAFFVWL-----FVCPMMRRKITGKLOKRGALSR- 254
QY 410 SIFDEQTSKALTJNWRNTAKEKKKVRDTMLMAQMGIDATPSRGSSPMPSRGSSP----- 463
DB 255 -VSDELSKVQEAESPVEKELPGAKANDSTIPLGAAGETLGTSEGTSGASHRAAYGR 313
QY 464 -----VHLHKGMRSD-----PQSAPTS 483
DB 314 ALSMTHGSVKSPISNGTFGFDGHTRSDGHVYHTVHKDSGLYKDLLHKIHIDRGPEKPAQ 373
QY 484 PRTQGEAR--DMYPPVVAH-----PVHRLNPNDRRRSASSALE 520
DB 374 ESNYRLLRNNSYTCYTAICGLPVHA-----TFRADSSAPE 411

RESULT 15
US-09-404-650-5

; Sequence 5, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1835
; TYPE: prt
; ORGANISM: Rattus sp.

US-09-404-650-5

Query Match 3.1%; Score 87; DB 4; Length 1835;
Best Local Similarity 18.8%; Pred. No. 8.3;
Matches 93; Conservative 74; Mismatches 153; Indels 174; Gaps 26;

QY 65 MLVGFISLLIVTQDPIIAKICISEDADVMWPCRGTEG-----RK 106
DB 1366 MLIFYISFLIVSEFVLNMFVG---VVENFHKCRQHOEAERREKRLRLLEKKRRK 1422
QY 107 PSK---YVDCPEGKVALMSTGSLHQLVFIYVAVFHVTVSVITIALSRKMRWKWE 163
DB 1423 AQRLPYATYCPY-RLLIHSMCTSHYIDIFI---TFIICLVNVTMSLEHYNQP----- 1472
QY 164 TETTSLEXQFANDPARFRTHTQTSFYKRNHGLSSTPGIRWVAF-FRQFPRSVTKVDYLT 222
DB 1473 SLETALKY-----CNMYFT--TVFY-----LEAVLKLVAFGURRFFKD----- 1508
QY 223 LRAGFINAHLSONSKFDFHKKYIKRSMEDDFKVVVIGISLPLMGVAITLFLDINGVGTLIW 282
DB 1509 -----RWNLDLAIVL---LSVMGITLEE--IEINAA----- 1535
QY 283 ISFIPVLICVGTGKLEMIIMEMALEIODRA---SVIKGAPVVEPSNKFVWFHPRDWLTF 339
DB 1536 LPINPTIIRIMYLRVARIARVLKLMATGMALLDVTVOALPOVGNIGLLE-----MLLF 1589
QY 340 FIFHLT-----FQNAFQMAHFVWTVAATPG-----LK 365
DB 1590 FIYAALGVELFGKLYCNDENPCEGMSRHATFEN-FGMAFLTLEFQVSTGDNWNGIMKDTLR 1648
QY 366 KCYHTQ-IGLSIMKVVVGLALQFLCSYMTFPLIYALYTOMGSNMKRSTFDEQTSKALTNR 424
DB 1649 DCTHDERTCLSSLOFVSPL---YFVSFVLTAQFVLINVVAVLMLKHLDSN-----K 1697
QY 425 NTAKKKKVRDTMLMAQMGID-----TPSRG-----SSP-MPSRGSSPVH 465
DB 1698 EAQEDAEMDAEIELEMAHGLGPCPGPCPCPCPCPCPCAGPRLPTSSPGAFGRGSG--- 1754
QY 466 LHKGMGRSDPOS 479
DB 1755 ----GAGAGDTEES 1764

Search completed: July 23, 2002, 14:25:22
Job time: 3295 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2002, 13:27:22 ; Search time 61.82 Seconds
(without alignments)
957.657 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPAPELPEPPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2788	100.0	533	19	AAW59442	Hordeum vulgare ML
2	2788	100.0	533	21	AAB03401	Barley MLO protein
3	2782	99.8	533	19	AAW59443	Hordeum vulgare ML
4	2434	87.3	534	21	AAB01805	Wheat MLO homologu
5	2433	87.3	534	20	AAV26966	Wheat MLO fungal r
6	2433	87.3	534	20	AAV26968	Wheat MLO fungal r
7	2433	87.3	534	22	AAB31250	Amino acid sequenc
8	2433	87.3	534	22	AAB31252	Amino acid sequenc
9	2432	87.2	534	20	AAV26967	Wheat MLO fungal r
10	2432	87.2	534	22	AAB31251	Amino acid sequenc
11	1927	69.1	544	19	AAW59445	Hordeum vulgare ML

12	1767.5	63.4	536	19	AAW59444	Oryza sativa MLO p
13	1257	45.1	515	20	AAV14139	Zea mays SCLBr pro
14	1257	45.1	515	21	AAV44605	Maize MLO6 protein
15	1253.5	45.0	573	20	AAV26970	Arabidopsis thalia
16	1253.5	45.0	573	21	AAV35698	Arabidopsis thalia
17	1253.5	45.0	573	22	AAB31254	Amino acid sequenc
18	1234.5	44.3	583	21	AAB03404	Arabidopsis thalia
19	1160	41.6	565	21	AAV44602	Maize MLO2 protein
20	1134.5	40.7	569	20	AAV26969	Arabidopsis thalia
21	1134.5	40.7	569	22	AAB31253	Amino acid sequenc
22	1130.5	40.5	593	20	AAV26972	Arabidopsis thalia
23	1130.5	40.5	593	22	AAB31256	Amino acid sequenc
24	1100	39.5	542	21	AAB03402	Arabidopsis thalia
25	1098	39.4	221	21	AAB01797	Wheat MLO homologu
26	1072	38.5	530	21	AAB01795	Soybean MLO homolo
27	1071.5	38.4	511	21	AAV35699	Arabidopsis thalia
28	998	35.8	482	21	AAV35700	Arabidopsis thalia
29	944	33.9	506	21	AAB01793	Soybean MLO homolo
30	932.5	33.4	526	19	AAW59446	Arabidopsis thalia
31	932.5	33.4	526	21	AAB03403	Arabidopsis thalia
32	927.5	33.3	526	22	AAB31255	Amino acid sequenc
33	924.5	33.2	526	20	AAV26971	Arabidopsis thalia
34	916	32.9	187	21	AAB01794	Arabidopsis thalia
35	888.5	31.9	492	20	AAV14135	Soybean MLO homolo
36	888.5	31.9	492	21	AAV44607	Zea mays SCLBr pro
37	887	31.8	492	21	AAB01808	Wheat MLO homologu
38	886	31.8	450	21	AAB01798	Wheat MLO homologu
39	801.5	28.7	496	21	AAV44782	Maize MLO3 protein
40	801.5	28.7	496	22	AAV00505	Maize disease resi
41	783.5	28.1	499	21	AAV44606	Maize MLO7 protein
42	765	27.4	224	21	AAV44601	Maize MLO1 protein
43	752.5	27.0	264	20	AAV14140	Zea mays SCLBr pro
44	730.5	26.2	509	20	AAV14138	Zea mays SCLBr pro
45	729.5	26.2	509	21	AAV44603	Maize MLO4 protein

ALIGNMENTS

RESULT 1	
AAW59442	
ID AAW59442	standard; Protein; 533 AA.
XX	
AC AAW59442;	
DT 13-OCT-1998	(first entry)
XX	
DE Hordeum vulgare MLO protein.	
XX	
KW MLO; mildew; pathogen; resistance.	
XX	
OS Hordeum vulgare.	
XX	
PN WO9804586-A2.	
XX	
PD 05-FEB-1998.	
XX	
PF 29-JUL-1997;	97WO-GB02046.
XX	
PR 07-MAR-1997;	97GB-0004789.
PR 29-JUL-1996;	96GB-0015879.
PR 30-OCT-1996;	96GB-0022626.
XX	
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.	
XX	
PI Bueschges R, Panstruga R, Schulzelefert PMJ;	
XX	
DR WPI; 1998-159149/14.	
DR N-PSDB; AAV35022.	
XX	
PT New isolated MLO gene of barley - used to develop products for the	
PT production of transgenic plants which have increased pathogen	
PT resistance	

XX AAM59443;
AC 13-OCT-1998 (first entry)
DT
XX Hordeum vulgare MLO protein.
DE
XX MLO; mildew; pathogen; resistance.
KM
XX Hordeum vulgare.
OS
XX WO9804586-A2.
PN
XX 05-FEB-1998.
PD
XX 29-JUL-1997; 97WO-GB02046.
PF
XX 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX WPI; 1998-159149/14.
DR N-PSDB; AAV35026.
XX
PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 7; 150pp; English.
XX
CC The sequence is that encoded by the MLO gene, wild-type MLO
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 533 AA;

Query Match 99.8%; Score 2782; DB 19; Length 533;
Best Local Similarity 99.8%; Pred. No. 4.8e-293;
Matches 532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSDKGVPARELPTPSWAVVAFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKM 60
Db 1 msdkgyvparelpetpswavavfamvlsvmlmehghlklghwfhkhalwealekm 60
QY 61 KAEMLVGFISLLIVTQDPIIAKICISEDADVMWPCCKRGTEGRKPSKYVDYCEGKYA 120
Db 61 kaelmvgfislilvtqdpilakicisedaadvmpckrgtegrkpskyvdycegya 120
QY 121 LMSTGSLHQLHVFIFVLAVFHVTVSVTITIALSRLKMRWKWMEETTSLEYQFANDPARF 180
Db 121 lmtsgslhqlhvlifvlavfhvtsvtitaisrlkmtwkkwetetstleyqfandparf 180
QY 181 RFTHTSFVKRHGLSSTPGIRWVAFFRQFFRSVTKVDTLTLRAGFINAHLSONSKRDF 240
Db 181 rfthtsfvkrhglstpgirwvaaffrqffrsvtkvdytltlragfinahlsgnskfd 240
QY 241 HKYIKRSMEDDFKVVVGISLPLMGVAITLPLDINGVGTLLWISFIPLVILLCVGTKLEM 300
Db 241 hkyikrsmmeddfkvvvgislplmgvaaitlpldingvgttlwisfipvlillcvgtklem 300
QY 301 IIMEMALEIODRASVIKGAPEVPEPSNKRFFWHRPDVLFELHLLTFQNAFQMAHFVWIVA 360
Db 301 iimemaleiodrasvikgapvepsnkrffwhrpdvlfelhlldtfqnafomahfvwtiva 360

Db 301 iimemaleiqdrasvlgapvpepsnkffwfhrrpdwvlfelhlldtfqnafqmahfvwtva 360
QY 361 TPGLKKCYHTOIGLSIMKVVVGLALQFLCSYMTPEPLVALVTOMGSNMKRSIFDEQTSKAL 420
Db 361 tpglkkcyhtqiglsimkvvgjalqflcsymtpeplvalvtqmgsmkrsifdeqtskal 420
QY 421 TNWRNTAKEKKKVRDMDLMAQMIGDATPSRGSSPMPSPRGSSPVHLHKGMRSDDPQSA 480
Db 421 tnwrntakekkkvrtdmdlmaqmigdatpsrgsspmpsrgrsspvhlhkgmrddpqsa 480
QY 481 PISPRTOGEARDMYPVVVAHPVHRLNPNDRRRSASSALAEADIPSADEFSGSOG 533
Db 481 ptsprtqgeardmypyvvahpvhrlnpndrrrsassaleadipsadefsfsqg 533

RESULT 4
AAB01805
ID AAB01805 standard; Protein; 534 AA.
XX
AC AAB01805;
XX
DT 27-OCT-2000 (first entry)
XX
DE Wheat Mlo homologue putative protein sequence #4.
XX
KW Wheat; Mlo homologue; disease resistance.
XX
OS Triticum aestivum.
XX
PN WO200036110-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US30181.
XX
PR 18-DEC-1998; 98US-0112737.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
DR WPI; 2000-431590/37.
DR N-PSDB; AAA52715.
XX
PT New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX
PS Claim 10; Page 64-66; 79pp; English.
XX
CC The present sequence is a putative protein sequence for a Mlo homologue
CC from wheat. Its coding sequence was identified by searching a root and
CC leaf cDNA library for sequences encoding proteins similar to Mlo from
CC Hordeum vulgare (barley) and Arabidopsis thaliana. Mlo confers resistance
CC to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation
CC leads to the priming of disease resistance even if the pathogen is not
CC present. The gene and protein can be used to create transgenic plants
CC which have increased disease resistance, as well as allowing researchers
CC to find other resistance-conferring genes and proteins.
XX
SQ Sequence 534 AA;

Query Match 87.3%; Score 2434; DB 21; Length 534;
Best Local Similarity 89.2%; Pred. No. 3.2e-255;
Matches 471; Conservative 20; Mismatches 33; Indels 4; Gaps 3;
QY 8 PARELPETPSWAVVAFAAMVLSVLMHGLHKLGHWFQHRHKKALWEALEKMAELMLV 67
Db 9 partlpetpswavaivfamivsvlllehalhklghwfhkthknaalealekmaelmlv 68
QY 68 GFISLLIVTQDPIIAKICISEDADVMWPCCKRGTEGRKPSKYVDY--CPEGVALMSTG 125
Db 69 gfislllavtqdp-igsicisekaasimprcsi-ppgsvkskykdyccakgkvslnstg 126

QY	126	SLHOLHVEFIVLAVFHVTVTSVITLALSRLKMRTWKKWETETTSLEYOFANDPARFRETTHQ	185
Db	127	slhqlhlfvflavfhtvtsvltmalstrlkmrtwkkweteasleyqfandparfittq	186
QY	186	TSFVKRHLGLSTPGIRWVAFFRQFFRSVTKVDYLLTRACFINAHLSONSKFDEFERYIK	245
Db	187	tsfvkrlhglstpgirwvafrqffrsvtckvdylltragfinahlshnskfdhkyik	246
QY	246	RSMEDDFKVVVGISLPLMGVAITLLELDINGVGTLLIWISFPLVILLCVGTKLEMIIMEM	305
Db	247	rsmeddffkvvgvislplmcvaaitllldldgltlwtwistflvlllcvgtkleimimem	306
QY	306	ALEIODRASVIGAPVVERPSNKEFWERHPDWLFFIHLTLFONAFQMAHFVWTVAETPGLK	365
Db	307	aleiodrasvixgapvverpsnkffwfrpdpwlffihltlfqnafqmahfwtvaetpglk	366
QY	366	KCYHTQIGLSIMKVVVGLAQFLCSYMTFPLYALVTOMGSNNKRSIFDEQTSKALTWNRN	425
Db	367	kcfmhthiglsimkvvglaqlgflcsytlfplyalvtqmgsmnkrsifdeqtakaltwnrn	426
QY	426	TAKEKKKVRDPTDMLMAOMIGDATPSRGSSPMPSRGSSPVHLLHKMGMSDDPOSAPNPR	485
Db	427	takekkkvrdctdmalmagmigdatspsrgtspmpsrasspvhlhkgmgrsddpqsaptspr	486
QY	486	TQOEARDMYPVVVAHPVHRLNPNDRRRSASSSALREADIPSADEFSFSG	533
Db	487	tmeearmdypvvvahpvhrlnpndrrrsasssalreadipsadesfsq	534

CC	XX	RESULT	5
CC	XX	AAV26966	
CC	XX	AAV26966	standard; Protein; 534 AA.
CC	XX	AAV26966;	
CC	XX	21-DEC-1999	(first entry)
CC	XX	wheat Mlo	funeral resistance protein Trm101.
CC	XX	Consensus;	resistance; fungus; pathogen; wheat; cell wall; apposition;
CC	XX	papilla;	contact site; callose; carbohydrate; phenol; transgenic plant;
CC	XX	Mlo;	Erysiphe graminis; powdery mildew.
CC	XX	Triticum	sp.
CC	XX	WO9947552-A2.	
CC	XX	23-SEP-1999.	
CC	XX	17-MAR-1999;	99WO-EP01779.
CC	XX	17-MAR-1998;	98US-0042763.
CC	XX	(NOVS)	NOVARTIS AG.
CC	XX	(NOVS)	NOVARTIS-ERFINDUNGEN VERW GES MBH.
CC	XX	Salmeron JM,	Weislo LJ, Strawn LJ, Kramer CM;
CC	XX	WPI;	1999-571820/48.
CC	XX	N-PSDB;	AAZ30409.
CC	XX	New proteins	useful for generating transgenic plants resistant to
CC	XX	funeral	infection
CC	XX	Claim 2;	Page 58-60; 102pp; English.

CC are used to generate transgenic plants resistant to fungal pathogens,
CC especially Erysiphe graminis (powdery mildew).
XX
SQ Sequence 534 AA;

Query Match	87.38;	Score 2433;	DB 20;	Length 534;
Best Local Similarity	88.28;	Pred. No. 4.1e-255;		
Matches 470; Conservative	22;	Mismatches 37;	Indels 4;	Gaps 3;

QY	3	DKKGVAPARELPETPSWAVAVVFAAVVAVSVLMEHGLHKLGHMFOHRHKKALWEALEEMKA	62
Db	4	ddeyppartlpetpswavalvfaamlvsvllehalhkiqhwfnhrkhnalaaelxika	63
QY	63	ELMLVGFISLULLIVTODPIIAKICISIEDAADVMWPCCKRGTEGRKPSKYVDY--CPEGKVA	120
Db	64	elmlvgfisl1lavtqdp-1sg1c1sekaasimrpck1-ppgsvkskykdycaqgkvs	121
QY	121	1MSTGSLHQLHVEIFVLAVFHVHTYVITIALSRLKMRTWKKMETETTSLEYOFANDPARF	180
Db	122	1mstgslhqlh1ffivlavfhvtyv1malsslkmtwkkwetetasleyqfandparf	181
QY	181	RETHQTSFVKRHLGLSSTPGIRWVVAFFEROFFRSVTKVDYITLRAGFINAHLSONSKEDF	240
Db	182	rftbqtsfvkrhlglstpgyrvwvaffrgffrsvtkvdyitlragfinahlsnshkfd	241
QY	241	HKYIKRSMEDBEKVVVGISLPIMGVALITLFLDINGVGTITWISFIPVLILCVGTELEM	300
Db	242	hkyikrsmmedbfkvvgislplwcvallt1fididg1gtlwis1fipvlilcvgteklem	301
QY	301	11EMALEIQDRAVVIKGA PVVERPSNKFWEFHRPDWVLF1HLTLFQNAFOMAHFVMTVA	360
Db	302	11emalaidqdrasv1kgapverpsnklf1fhrpdwvlf1hl1l1fyna1fma1fwtva	361
QY	361	TPGLKKCYHTQIGLSIMKVVVGLADPLCSYMTFPL1YALVYOMGSMNKRIS1FDEQTSKAL	420
Db	362	tpglkkcfhmh1gisimkvvlg1alq1csy1t1fpl1yalvtqmgsmnkris1fdeqtakal	421
QY	421	TNWRNTAKEKKKVVYD1DMLMAQMG1DATPSRGSSPMPSPRGSSPEVHL1HKGMGRSDPOSA	480
Db	422	tnwrntakekkkvvrd1dmlmagm1gdat1psrgaspm1psrgsspvhl1hkmg1grsd1p1st	481
QY	481	PTSPRTQOEARDM1PVVVAHPVHRLNPNDRRKSASSSAL1EAD1PSADFSFQSG	533
Db	482	ptsp1rteeardm1pvvva1hpv1h1npad1rr1svssal1dvad1psad1fs1sg	534

RESULT	6	
AAV26968		
ID	AAV26968	standard; Protein; 534 AA.
XX		
AC	AAV26968;	
XX		
DT	21-DEC-1999	(first entry)
XX		
DE	Wheat Mlo	fungal resistance protein Trmlo3.
XX		
KW	Consensus;	resistance; fungus; pathogen; wheat; cell wall; apposition;
KW	papilla;	contact site; callose; carbohydrate; phenol; transgenic plant;
KW	Mlo;	Erysiphe graminis; powdery mildew.
XX		
OS	Triticum	sp.
XX		
PN	WO9947552-A2.	
XX		
PD	23-SEP-1999.	
XX		
PF	17-MAR-1999;	99WO-EF01779.
XX		
PR	17-MAR-1998;	98US-0042763.
XX		
PA	(NOVS)	NOVARTIS AG.
PA	(NOVS)	NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
PI WPI; 1999-571820/48.
XX DR N-PSDB; AA230411.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 68-70; 102pp; English.
XX
CC This sequence represents the wheat fungal resistance protein TrM1o3,
CC which confers resistance to fungal pathogens by stimulating the formation
CC of large cell wall appositions, designated papillae, at the contact site
CC with the fungal pathogen. These papillae mainly contain callose, but
CC also contain carbohydrate, phenols and proteins and are used to prevent
CC penetration of the fungal hyphae into the plant. The new M1o sequences
CC are used to generate transgenic plants resistant to fungal pathogens,
CC especially Erysiphe graminis (powdery mildew).

XX Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 20; Length 534;
Best Local Similarity 88.8%; Pred. No. 4.1e-255;
Matches 469; Conservative 22; Mismatches 33; Indels 4; Gaps 3;

OY 8 PARELPETPSWAVAVFAAMVIVSVLMHGLHKLGHWFQHRHKKALWEALEKKMAELMLV 67
DB 9 partlpetpswavalvafamliysvlllehalhklghwfhrkhknaalekmaelmlv 68
OY 68 GFISLLIVTODPIIAKICISEDADVMWPCRGTEGRKPSKYVDY--CPEGKVALMSTG 125
DB 69 gfislllavtqdp-1sgicisqkaasimrpck-vepgsvkskykdyccakegkvalmstg 126
OY 126 SLHQLHVFIFVLAVFHVTVSVITIALSRCLKMRTWKWETETTSLEYQFANDPARFRFTHQ 185
DB 127 slhqlhifflavfhvtysvilma1sr1kmtwtkwetetasleyqfandparfrfthq 186
OY 186 TSFVKRHLGLSTPGIRWVVAEFRQFRSVTKVDYLTLRAGFINAHLSONSKFDFHKYIK 245
DB 187 tsfvkrhlglstpgvrwvvafrqffrsvtkvdyltlragfinahlsqnskfdfhkyik 246
OY 246 RSMEDFRVVGISLPLMGVAITLFLDINGVGTLMWISFIPVLILCVGTKLEMIIMEM 305
DB 247 rsmedfrvvgislpwava1ltflididig1gtltwvsfip1ililcvgtkleimimgm 306
OY 306 ALEIQDRASVIKGA PVVEPSNKFEPWRHPDWLFFIH1TLFQNAEQMAHFVWTVATPGLK 365
DB 307 aleiqdrsv1kga pvvepsnklfwhrpdwv1lffih1tlfqnaeqmahfwtvatpglk 366
OY 366 KCVHTQIGISIMKVVVGLAQFLCSYMTFPLALVTOMGSNMKRSIPDEQTSKALTNRN 425
DB 367 dcfhm1g1simkv1glalqflcsy1t1p1yalvtqmgsmkrsifdeq1akalt1nrn 426
OY 426 TAKEKKKVRDPTMLMAQMITGATPSRGSSPMPSRGSSPVHLHKMGMSDDPQSAPTS PR 485
DB 427 takekkvrdctmlmagmitgatsrgtspmsrgsspvhl1qkgmgsddpqsaptspr 486
OY 486 TQOEARDMYPVVAHPVHRLNPNDRRRSASSALEADIPSA DFSFSQ 533
DB 487 tmeearm1p1vva1hpvhrlnpndrrrsassaleadipsadfsfsq 534

RESULT 7
AAB31250
ID AAB31250 standard; Protein; 534 AA.
XX AAB31250;
AC
XX 20-APR-2001 (first entry)
DT
XX Amino acid sequence of the wheat M1o protein TrM1o1.
DE

XX Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW powdery mildew; M1o; cell wall apposition; transgenic plant.
XX
OS Triticum sp.
XX
PN WO200078799-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-EP05576.
XX
PR 18-JUN-1999; 99US-0336112.
XX

PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernooij BT, Levin JZ, Heifetz PB, Patton DA, Que Q;

DR WPI; 2001-112311/12.
DR N-PSDB; AAF24583.

PT Novel polynucleotide which encodes M1o protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
XX Claim 12; Page 90-92; 128pp; English.

XX The present sequence represents a M1o protein. M1o proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC M1o proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the M1o
CC locus are responsible for a plant resistant phenotype. The mechanism
CC of M1o resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding M1o proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.

SQ Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 22; Length 534;
Best Local Similarity 88.2%; Pred. No. 4.1e-255;
Matches 470; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

OY 3 DKKGVARELPETPSWAVAVFAAMVIVSVLMHGLHKLGHWFQHRHKKALWEALEKKMA 62
DB 4 ddeyppartlpetpswavalvafamliysvlllehalhklghwfhrkhknaalek1ka 63
OY 63 ELMVGFISLLIVTODPIIAKICISEDADVMWPCRGTEGRKPSKYVDY--CPEGKVA 120
DB 64 elm1vgfislllavtqdp-1sgicisekaasimrpck1-ppgsvkskykdyccakgkvs 121
OY 121 LMSTGSLHQLHVFIFVLAVFHVTVSVITIALSRCLKMRTWKWETETTSLEYQFANDPARF 180
DB 122 l1mstgslhqlhifflavfhvtysvilma1sr1kmtwtkwetetasleyqfandparf 181
OY 181 RFTHTQSFVKRHLGLSTPGIRWVVAEFRQFRSVTKVDYLTLRAGFINAHLSONSKFDF 240
DB 182 rfthtqsfvkrhlglstpgirwvvafrqffrsvtkvdyltlragfinahlsnkskfd 241
OY 241 HKYIKRSMEDFRVVGISLPLMGVAITLFLDINGVGTLMWISFIPVLILCVGTKLEM 300
DB 242 hkyikrsmedfrvvgislpwava1ltflididig1gtltwvsfip1ililcvgtkle1m 301
OY 301 IIMEMALEIQDRASVIKGA PVVEPSNKFEPWRHPDWLFFIH1TLFQNAEQMAHFVWTV 360
DB 302 i1memaleiqdrasv1kga pvvepsnklfwhrpdwv1lffih1tlfqnaeqmahfwtva 361
OY 361 TPGLKKCYHTQIGLSIMKVVVGLAQFLCSYMTFPLALVTOMGSNMKRSIPDEQTSKAL 420
DB 362 tpglkkcfh1m1g1simkv1glalqflcsy1t1p1yalvtqmgsmkrsifdeq1akal 421

QY 421 TNWRNTAKEKKVVDTDMLAOMIGDAPSRGSSPMPSPRGSSPVHLLHKMGSRDDPSQA 480
DB 422 twnrtakekkvrdtdmlmagmigdatsrgaspmprsgspvhlhkgmgsddpqt 481
QY 481 PTPSPRTOGEARDMPVVAHPVHRLNPNDRRRSASSALEADIPSADFSQSOG 533
DB 482 ptpspmeardmvpvvaahpvrhlnpdrrrsvssaldvdpidsadfsqs 534

RESULT 8

AAB31252
ID AAB31252 standard; Protein; 534 AA.

AC AAB31252;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of the wheat Mlo protein Trm103.

KW Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;

KW powdery mildew; Mlo; cell wall apposition; transgenic plant.

OS Triticum sp.

PN WO200078799-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000WO-EP05576.

PR 18-JUN-1999; 99US-0336112.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;

PI Vernooij BT, Levin JZ, Heifetz PB, Patton DA, Que Q;

DR WPI; 2001-112311/12.

DR N-PSDB; AAF24585.

PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
producing fungal resistant plants, in particular wheat plant

PS Claim 12; Page 99-101; 128pp; English.

CC The present sequence represents a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant pathotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.

XX Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 22; Length 534;
Best Local Similarity 88.8%; Pred. No. 4.1e-255;
Matches 469; Conservative 22; Mismatches 33; Indels 4; Gaps 3;

QY 8 PARELPETPSNAVAVFAAMVLSVMEHGLHKLGHWFQHRHKKALMEALEKMAELMLV 67

DB 9 partlpetpswavalvafamvlsvlehalhklghwfhkhrhnaaleakmkaelmlv 68

QY 68 GFISLLIVTQDPIIAKICISEDADAVMWPCKRGTEGRKPSKYVDY--CPEGVALMSTG 125

DB 69 gfislllavtcqp-lsgiclsqkaaslmprck-vepgsvkskykdyycakegkvalmstg 126

QY 126 SLHQLHVEIFVLAVEHVTSVITIALSRLLKMTWKWETETTSLEYQFANDPARFRFTHQ 185
DB 127 slhqlhffifvlavfhtvsvilmaalsrlkmtwkwtetasleyqfandparfrfthq 186
QY 186 TSFVKRHLGISTPGIRWVAFFRQFRRSVTKVDYLTLRAGFINAHLSONSKDFHKKYIK 245
DB 187 tsfvkrhlglstpgirwvaftrqfrrsvtkvdyltragfinahlsqnskfthkyik 246
QY 246 RSMEDDFKVVVGLSLPLMGVAITLFLDINGVGTLLWISFIPVLILCVGTKLEMIIMEM 305
DB 247 rsmeddfkvvgvlslplmgvailtflldingvgtllwvsfipvlilcvgtklemlimgm 306
QY 306 ALEIQDRASVIKGAPEVPEPSNKEFEHFRPDWVLFETHTLTFQNAFQMAHFVWVAATPGLK 365
DB 307 aleiqdrsvlkgapevpepsnkffwfrpdwvlfethtltnaafqmahfvtvatpglk 366
QY 366 KCIHTQIGISIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMRSIFDEQTSKALTNRN 425
DB 367 dcfhmniqslmkvvlglalqflcsyftfplyalvtqmgsumkrsifdeqtakaltwnr 426
QY 426 TAKEKKVVDTDMLAOMIGDAPSRGSSPMPSPRGSSPVHLLHKMGSRDDPSQAPTS 485
DB 427 takekkvrdtdmlmagmigdatsrgtspmpsrsgspvhlhkgmgsddpqsaptspr 486
QY 486 TQGEARDMPVVAHPVHRLNPNDRRRSASSALEADIPSADFSQSOG 533
DB 487 tmeardmvpvvaahpvrhlnpdrrrsvssaldvdpidsadfsqs 534

RESULT 9

AA26967
ID AA26967 standard; Protein; 534 AA.

AC AA26967;

DT 21-DEC-1999 (first entry)

DE Wheat Mlo fungal resistance protein Trm102.

KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;

KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;

KW Mlo; Erysiphe graminis; powdery mildew.

OS Triticum sp.

XX Key Location/Qualifiers

XX Misc-difference 168 /label- unknown

PN WO9947552-A2.

PD 23-SEP-1999.

PF 17-MAR-1999; 99WO-EP01779.

PR 17-MAR-1998; 98US-0042763.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;

DR WPI; 1999-571830/48.

DR N-PSDB; AAZ30410.

PS Claim 2; Page 63-65; 102pp; English.

XX This sequence represents the wheat fungal resistance protein Trm102,
CC which confers resistance to fungal pathogens by stimulating the formation

CC of large cell wall appositions, designated papillae, at the contact site
CC with the fungal pathogen. These papillae mainly contain callose, but
CC also contain carbohydrate, phenols and proteins and are used to prevent
CC penetration of the fungal hyphae into the plant. The new Mlo sequences
CC are used to generate transgenic plants resistant to fungal pathogens,
CC especially Erysiphe graminis (powdery mildew).

XX Sequence 534 AA;

Query Match 87.2%; Score 2432; DB 20; Length 534;
Best Local Similarity 89.2%; Pred. No. 5.3e-255;
Matches 471; Conservative 20; Mismatches 33; Indels 4; Gaps 3;

QY 8 PARELPETPSWAAVVAFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKKAELMLV 67
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 partlpetswavalvfaamlivsvlllehalhklghwfhkrhknalaalekikaelmly 68

QY 68 GFISLLIIVTODPIIAKICISEDADAVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 gfislllavtqdp-|sgicisekaasimprcs|-ppgsvkskykdyckakgkslmstg 126

QY 126 SLHQLHVFIFVLAVFHVHTYSVTTIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 slhqlhmffivlavfhtyvimalsrklmrkwtetetsleyqfandparfrfthq 186

QY 186 TSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLTRAGFINAHLSONSKRDFHKKYIK 245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 tsfvkrhlglstpgirwvvafrqfrsvtkvdylltragfinahlsnskdfhkyik 246

QY 246 RSMEDDFKVVVGISLPLMGVAIITLFLDINGVGLIWIISFIPVILLCVGTKEIIMEM 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 247 rsmeddfkvvgislpwcvailtlfldidgltlwisfipvlilcvgtkleimimem 306

QY 306 ALEIQDRASVIKGAPEVPSNKFEFWHRPDWVLEFTHLTLFONAFQMAHFVTVATPGLK 365
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 307 aleiqdrasvikgapvepsnkffwhrpdwvlfthltlfnafqmahfvwtvatpglk 366

QY 366 KCYHTQIGLSIMKVVGIALQFLCSYMTFPLVALVTQGSNMKRSIFDEQTSKALTNRN 425
||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 367 kcfhmhiglsimkvvgialqficsyitfplvalvtqgsmnkrsifdeqtakaltwnr 426

QY 426 TAKEKKKVRDTMLMAQMGIDATPSRGSSPMPSPRGSSPVHLHKGMSDDPOSAPTSR 485
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 427 takekkkvrtdmlmaqmgidatpsrgtspmraspvhllhkgmsddpqsaftspr 486

QY 486 TQGEARDMYPVVVAHPVHRLNPNDRRRSASSSALADIPSADFSFSQG 533
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 487 tmeearmypyvvahpvhrlnpndrrrsassaldadipsadfsfsqg 534

RESULT 10
AAB31251
ID AAB31251 standard; Protein; 534 AA.
XX
AC AAB31251;

XX 20-APR-2001 (first entry)
XX
DE Amino acid sequence of the wheat Mlo protein TrMlo2.
XX
KW wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW powdery mildew; Mlo; cell wall apposition; transgenic plant.
XX
OS Triticum sp.

XX Key Location/Qualifiers
FH Misc-difference 168
FT /note- "unspecified amino acid encoded by GYC"
XX
XX WO200078799-A2.
XX
PD 28-DEC-2000.

XX 16-JUN-2000; 2000WO-EP05576.
PF
XX
PR 18-JUN-1999; 99US-0336112.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernoolj BT, Levin JZ, Helfetz PB, Patton DA, Que O;
XX
DR WPI; 2001-112311/12.
DR N-PSDB; AAF24584.
XX
PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
PS Claim 12; Page 94-96; 128pp; English.

XX Sequence 534 AA;

Query Match 87.2%; Score 2432; DB 22; Length 534;
Best Local Similarity 89.2%; Pred. No. 5.3e-255;
Matches 471; Conservative 20; Mismatches 33; Indels 4; Gaps 3;

QY 8 PARELPETPSWAAVVAFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKKAELMLV 67
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 9 partlpetswavalvfaamlivsvlllehalhklghwfhkrhknalaalekikaelmly 68

QY 68 GFISLLIIVTODPIIAKICISEDADAVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 69 gfislllavtqdp-|sgicisekaasimprcs|-ppgsvkskykdyckakgkslmstg 126

QY 126 SLHQLHVFIFVLAVFHVHTYSVTTIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 slhqlhmffivlavfhtyvimalsrklmrkwtetetsleyqfandparfrfthq 186

QY 186 TSFVKRHLGLSTPGIRWVVAFFRQFRSVTKVDYLLTRAGFINAHLSONSKRDFHKKYIK 245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 tsfvkrhlglstpgirwvvafrqfrsvtkvdylltragfinahlsnskdfhkyik 246

QY 246 RSMEDDFKVVVGISLPLMGVAIITLFLDINGVGLIWIISFIPVILLCVGTKEIIMEM 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 247 rsmeddfkvvgislpwcvailtlfldidgltlwisfipvlilcvgtkleimimem 306

QY 306 ALEIQDRASVIKGAPEVPSNKFEFWHRPDWVLEFTHLTLFONAFQMAHFVTVATPGLK 365
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 307 aleiqdrasvikgapvepsnkffwhrpdwvlfthltlfnafqmahfvwtvatpglk 366

QY 366 KCYHTQIGLSIMKVVGIALQFLCSYMTFPLVALVTQGSNMKRSIFDEQTSKALTNRN 425
||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 367 kcfhmhiglsimkvvgialqficsyitfplvalvtqgsmnkrsifdeqtakaltwnr 426

QY 426 TAKEKKKVRDTMLMAQMGIDATPSRGSSPMPSPRGSSPVHLHKGMSDDPOSAPTSR 485
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 427 takekkkvrtdmlmaqmgidatpsrgtspmraspvhllhkgmsddpqsaftspr 486

QY 486 TQGEARDMYPVVVAHPVHRLNPNDRRRSASSSALADIPSADFSFSQG 533
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 487 tmeearmypyvvahpvhrlnpndrrrsassaldadipsadfsfsqg 534

KW antifungal; antihelminthic; anti-arthropod; maize; HvMLO1.
XX
OS Zea mays.
FH Key Location/Qualifiers
FT Region 1..18
FT Domain /label= N-terminal_region
FT Domain /label= Transmembrane_helix_1
FT Region 37..65
FT Domain /label= Intervening_region_1
FT Domain /label= Transmembrane_helix_2
FT Region 90..189
FT Domain /label= Intervening_region_2
FT Domain /label= Transmembrane_helix_3
FT Region 210..311
FT Domain /label= Intervening_region_3
FT Domain /label= Transmembrane_helix_4
FT Region 331..337
FT Domain /label= Intervening_region_4
FT Domain /label= Transmembrane_helix_5
FT Region 355..435
FT Domain /label= Intervening_region_5
FT Domain /label= Transmembrane_helix_6
FT Region 460..515
FT Region /label= C-terminal_region
XX
PN WO200001722-A1.
XX
PD 13-JAN-2000.
XX
PD 07-JUL-1999; 99WO-US15255.
XX
PF 07-JUL-1998; 98US-0091875.
XX
PR (PION-) PIONEER HI-BRED INT INC.
XX
PA Briggs SP, Simmons CR;
XX
PI WPI; 2000-137196/12.
XX
DR N-PSDB; AAZ49564.
XX
DR
XX
PT Creating or enhancing disease resistance in plants by modulating plant
PT resistance genes expression
XX
PS Claim 1b; Page 71-73; 88pp; English.
XX
CC The present sequence is the maize MLO6 (ZmMLO6) protein, which exhibits
CC sequence homology to barley MLO1 (HvMLO1) sequence. MLO6 protein is
CC encoded by a mutation-induced recessive allele Mlo6, located on
CC chromosome 5, that confers resistance to plant pathogens. Expression of
CC native MLO genes in plants can be altered by transforming them with a
CC DNA construct comprising the mutated Mlo gene. Decreasing the expression
CC or activity of native MLO protein leads to enhanced resistance of plants
CC against pathogens such as fungi, virus, nematodes and insects. Mlo gene
CC can be used to isolate related sequences from other plants and as
CC molecular markers used in breeding programs aimed at improving disease
CC resistance. MLO protein has anti-infective, antipathogenic, antiviral,
CC antifungal, antihelminthic and anti-arthropod activity.
XX
SQ Sequence 515 AA;

Query Match 45.1%; Score 1257; DB 21; Length 515;
Best Local Similarity 48.7%; Pred. NO. 2.6e-127;
Matches 251; Conservative 84; Mismatches 116; Indels 64; Gaps 7;

OY 6 GVPARELPETPSNAVAVFAAMVLVSLMEHGLHKLGHWFQHRHKKALWEALEKMAELM 65

Db 7 ggnstreldqptwavasvcgvilvllsillekylhvgelfshtrkkamvealekvkaelm 66
OY 66 LVGFISLLIVTQDPIIAKICISEDADVMWPCK-----RGTE----- 103
Db 67 vlgfisl1lvfgnyli-kvcisnhaantlmpckleaavegkdghgkeaaavagkxkv 125
OY 104 -----GRKPSK-----YVDY-----CPEGKVALMSTGSLH 128
Db 126 avavpgkrrkkkaaaadhlgyvvdwpppyahnaarmlaeasmatkcepgkvp1lsinalh 185
OY 129 QLHVFTFVLAVFHVTVYSVITIALSRKMRWKWETETTSLEYOFANDPARFRTHQTSF 188
Db 186 qlhiflflavfhvsysaitmalgraklrwkekeagaqdyetsndptrfrfthetsf 245
OY 189 VKRHLG-ISSTPGIRWVAVFRRQFFRSYTKVDYLTLRAGFINAHLSONSKFDFHKYIKRS 247
Db 246 vrqhmuvlnkfpasfysnffrqffrsvrqadycalrhsfvnvhlapskfdfqyikrs 305
OY 248 MEDDEKVVVGISLPLMGVAILTFLDINGVGTLIWISFIPVLVLLCVGTKLEMIEMAL 307
Db 306 ledffkvivgispplwasalifflnvngwhmlwisimpvillsvgtklglicrmai 365
OY 308 EIQDRASVIKGAPEVPSNKEFFWHRPDVWLFPIHLTLFONAFOMAHFVTVATPGLKKC 367
Db 366 diterhavigqipmwqvsdsyfwfartptfvlihfliifqngfqiylwilyeygmasc 425
OY 368 YHTQIGLSIMKVVVGLAQFLCSYMTFPLVAVTOMGSNMKRSIFDEQTSKALTNRNTA 427
Db 426 fndseefvarlclgyvvvqvlcsyvtlplyalvsgmstmkgsifdeqtskalknwraga 485
OY 428 KEKKKVRDITMLMAQMIGDATPSRGSSPMPSSRGSS 462
Db 486 kkkaptgy-----skhggygsptaggsptkdgda 515

RESULT 15
AAZ26970
ID AAY26970 standard; Protein; 573 AA.
XX
AC AAY26970;
XX
DT 21-DEC-1999 (first entry)
XX
DE Arabidopsis thaliana fungal resistance protein CIB10295.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW MLO; Erysiphe graminis; powdery mildew.
XX
OS Arabidopsis thaliana.
XX
PN WO9947552-A2.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI; 1999-571820/48.
DR N-PSDB; AAZ30413.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 3; Page 78-81; 102pp; English.
XX

CC This sequence represents the *Arabidopsis thaliana* fungal resistance
CC protein CIB10295, which confers resistance to fungal pathogens by
CC stimulating the formation of large cell wall appositions, designated
CC papillae, at the contact site with the fungal pathogen. These papillae
CC mainly contain callose, but also contain carbohydrate, phenols and
CC proteins and are used to prevent penetration of the fungal hyphae into
CC the plant. The new Mlo sequences are used to generate transgenic plants
CC resistant to fungal pathogens, especially *Erysiphe graminis* (powdery
CC mildew').

SQ Sequence 573 AA;

Query Match	45.0%;	Score 1253.5;	DB 20;	Length 573;
Best Local Similarity	44.1%;	Pred. No. 7.5e-127;		
Matches 261;	Conservative 91;	Mismatches 161;	Indels 79;	Gaps 13;

```

QY 1 MSCKGVPAARELPETPSMAVAVVEAAMVLSVLMEHGLHKLGHWFQHRHKAALWEALEKM 60
Db 1 madq--vkertleetstwavavvcfvllfislvslnhklgtwfkxkhhqalfealekv 58
QY 61 KAEMLVGFISLLIVTQDPIIAKICISEDADVMWPCCKRGTEGRKPSK----- 109
Db 59 kaelmlglfisliltigtpr-lslnctsqkvastmbpcsaeeakkgykkdagkkddgdg 117
QY 110 -----YV-----DYCPE-GKVALMSTGSLHQLHVFIFYLAVEHVTY 144
Db 118 dkpgrrlllelaesyihrrslatckgydkcaekgkvaafvsaygihqhlfflvavhvvy 177
QY 145 SVITIALSRLKMRTWKWKWETETTSLEYOFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
Db 178 civtyafigkikmrtwksweetktiegygsndperfrfardtsfgrnhlfnwsktrvtlw 237
QY 204 VVAFFRQFFRSVTKVDYLLTRAGFINAHL--QNSKFDFHKYIKRSMEDDERVWVGISLP 261
Db 238 lwcfcfrqfgsvtkvdylalrhgfmahfapgnesrfdfrkyigrslckdfktveispy 297
QY 262 LMGVAAILTLFLDINGVGTLIWISIFPLVILLCVGTKLEMITMEMALEIQDRAVYIKGAPV 321
Db 298 lwfvaavlfliltnsyglrsylwlpflvlvllivgtkleviltkligrigekgdvvrqgav 357
QY 322 VEPSNKFWEHRPDWVLFELHLEFQNAFQMAHFVWTVATPGLKKCYHIOGILSIMGVVV 381
Db 358 vqpgddlwfqkprfilflhlvlfenaqlaflawstyefnlnncfhestadvlrlvv 417
QY 382 GLALQELCSYMTFPLYALVWQSGNSMKRSIFDEQTSKALTNRNTAKEKKKYRDTMLMA 441
Db 418 gavgqlcsyvtlplyalvtqmgskmptvfndrvatalkkwhhtaknekk-----hg 470
QY 442 QMIGDATPSRGSSPMPSSRGSSPVHLHLKGMGRSDDPQASAPTSPTQGEARDMYPVVAHP 501
Db 471 rhsgsntpfssrptlptlhngssplhlhlnfnurs--venypsspsprysgh-----ghn 521
QY 502 VHRH-NPNDRRRSASSS-----ALEADIP-----SADFSSQ 532
Db 522 ehqfwdpesqhqaeatsthslaheseevlasvelpirtskslrdfsfxk 573

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Search completed: July 23, 2002, 14:24:34
Job time: 3432 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 09:00:27 ; Search time 1677.27 Seconds
(without alignments)
12891.259 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcgcgacaaaaagggt.....tttccttcagccagggatga 1602

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ESR:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	696.8	43.5	700	10	BE519781	BE519781 HV_CEB002
2	583.2	36.4	669	9	AV945501	AV945501 AV945501
3	581	36.3	605	9	AV835197	AV835197 AV835197
4	556	34.7	798	10	BE558835	BE558835 HV_CEB002
5	410	25.6	613	10	BE419320	BE419320 WMR06.F5R
6	402.2	25.1	536	10	BE405266	BE405266 WHE1210_E
7	395.8	24.7	402	9	AV945620	AV945620 AV945620
8	343.2	21.4	490	10	BG904891	BG904891 Talr1135F
9	284.8	17.8	688	10	BI954631	BI954631 HVSME001
10	253	15.8	773	10	BI808093	BI808093 C002D08 O
11	204.6	12.8	518	10	BG904890	BG904890 Talr1135F
12	203.4	12.7	408	9	AV835211	AV835211 AV835211
13	192.6	12.0	620	10	BG642916	BG642916 EST511110
14	191	11.9	643	10	BI432930	BI432930 EST535691
15	190.2	11.9	599	9	AM934153	AM934153 EST359996
16	188	11.7	663	10	BM080281	BM080281 MEST106-D
17	185	11.5	423	10	BF729342	BF729342 1000076C0

18	179.2	11.2	464	9	AL387000	AL387000 MtBC39D06
19	161.2	10.1	735	10	BI931548	BI931548 EST551437
20	158.8	9.9	615	10	BI922441	BI922441 EST542345
21	158.8	9.9	665	10	BI923467	BI923467 EST543372
22	152.8	9.5	598	9	BE020055	BE020055 sm38e01.Y
23	149	9.3	708	10	BG649130	BG649130 EST510749
24	147.8	9.2	447	10	BF587392	BF587392 FM1_35_G0
25	145.2	9.1	545	9	BE025314	BE025314 945028C09
26	145.2	9.1	761	10	BG130233	BG130233 EST475879
27	143	8.9	707	10	BM410789	BM410789 EST585116
28	137.8	8.6	576	9	AI993856	AI993856 701515174
29	137.2	8.6	849	10	BI309518	BI309518 EST530928
30	134.4	8.4	440	10	BF096305	BF096305 EST360354
31	133	8.3	605	9	AM216578	AM216578 EST295292
32	131.8	8.2	636	10	BM359705	BM359705 GA_Ea002
33	131.4	8.2	622	9	AI729603	AI729603 BNLGH1137
34	131.2	8.2	628	9	AI729043	AI729043 BNLGH1124
35	130.8	8.2	471	10	BE636983	BE636983 WHE1808_C
36	129	8.1	622	9	AI731933	AI731933 BNLGH1114
37	126.8	7.9	585	10	N37544	N37544 18771 Lambd
38	122.6	7.7	523	10	BI126403	BI126403 1075P03P
39	120	7.5	410	10	BM409501	BM409501 EST583828
40	119.8	7.5	456	10	BG132655	BG132655 EST465547
41	116.8	7.3	569	10	BE354015	BE354015 EST355358
42	116.2	7.3	456	9	AM132264	AM132264 sg98f11.Y
43	114.6	7.2	394	9	AV536614	AV536614 AV536614
44	114.2	7.1	447	9	AM132268	AM132268 sg98g11.Y
45	112.2	7.0	688	9	AV836759	AV836759 AV836759

ALIGNMENTS

RESULT 1
LOCUS BE519781 700 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEB0021D05f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEB0021D05f, mRNA sequence.

ACCESSION BE519781
VERSION BE519781.2 GI:13266203
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 700)

Wing,R., Close,T.J., Kleinbofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library

Unpublished (2001)
On Aug 8, 2000 this sequence version replaced gi:9743969.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases - 586
Seq primer: AATTAACTCTCACTAAAGG
High quality sequence start: 4
High quality sequence stop: 664.
Location/Qualifiers
1..700
/organism="Hordeum vulgare"
/cultivar="C16151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEB0021D05f"

FEATURES
source

/clone_lib="Hordeum vulgare seedling green leaf EST library HVCNDA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; C.I. 16151 (Mla6) plants were greenhouse grown in the R green lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the Tj Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close Tj, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/dgn/31/cover.html>)"

BASE COUNT 149 a 210 c 191 g 150 t
ORIGIN

Query Match 43.5%; Score 696.8; DB 10; Length 700;
Best Local Similarity 99.7%; Pred. No. 1.4e-124;
Matches 698; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 280 gtcatgtgacctgcaagcgcgaccgagggccgaagcccaagcaagtactgtactac 339
Db 1 GTCATGTGGCCTTGCAGCGCGGACCGGCGCCGCAAGCCAGCAAGTACTGTACTAC 60
OY 340 tggccggagggaaggtggtggtcatgttcaacgggcaagcttgaccagctgactctc 399
Db 61 TGCCCGGAGGGAAGGTGGCGCTCATGTCCAGCGGAGCTTGACACAGCTGACGTTCTT 120
OY 400 atcttcgtgtcggtcttccatgttcaactacagcgtcatcacatagctctaagcgt 459
Db 121 ATCTTGCTGCTGGGCTTCCATGTCACTACGCGTATCATCACATAGCTTAAGCCGT 180
OY 460 ctcaaatgagaacatggaagaatggtgagacagagaccacctcttggaataccagttc 519
Db 181 CTCAAATGAGAACATGGAAGAAATGGAGACAGACCACTCTTGGAATACAGTTTC 240
OY 520 gcaaatgatcctgcaaggttccggttcaacgacacagacgttctgtgaagcgccacctg 579
Db 241 GCAAAATGATCTTCACGGTTCGGTTCACGACACGACGTCGTTGTGAAGCGCCACCTG 300
OY 580 ggcctctccagcacccttgcatcagatggtgtggtccttctcaaggcagttcttcagg 639
Db 301 GGCCCTTCAGCACCCCTGGCATCAGATGGGTGGGCTTCTTCAGGACAGTTCTTCAGG 360
OY 640 tcagtcaccaaggtgactacactgacctgagggcaggtcttcaacgscgacttgtcg 699
Db 361 TCAGTCACCAAGGTGACTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTGCG 420
OY 700 caaacagcaagttcgacttccacaagtatcatcaagaggtcgatgagagcagctcaag 759
Db 421 CAAAACAGCAAGTTCGACTTCACACAAGTACATCAAGAGGTGATGAGAGCAGACTTCAAG 480
OY 760 gtcgtcgtcgcatcagcctcccgctgtgtgtgtgagatcctcaaccctcttcctgac 819

|||||
Db 481 GTCGTCGTGGCATCA6CCTCCCGCTGTGGGGTGTGGCGATCTCTACCCCTCTTCCTTGAC 540
OY 820 atcaatggttgacagcgtcatctgtgattcttctatccctctcgtatcctctgtgt 879
Db 541 ATCAATGGGTTGGCAGCGCTCATCTGATTTCTTCATCCCTCTCGTGAATCTCTGTGT 600
OY 880 gtggaaccaagctgagatgatcatcatgagatggccctgagatcccaagccggcg 939
Db 601 GTTGAACCAAGCTGAGATGATCATCATGAGATGGCCCTGAGATCCAAGACGGGCG 660
OY 940 agcgtcatcaaggggccccctgtgtcgagcccaaca 979
Db 661 AGCGTCATCAAGGGGGCCCCGTGTGTCAGCCAGCCAGCACCA 700

RESULT 2
AV945501/c 669 bp mRNA linear EST 18-JAN-2002
LOCUS AV945501 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone bah26013 3', mRNA sequence.

ACCESSION AV945501 GI:18241298
VERSION AV945501.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 669)
AUTHORS Sato, K., Saisho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin1@genes.nig.ac.jp.

FEATURES
source 1. .669
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah26013"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"

BASE COUNT 131 a 182 c 192 g 163 t
ORIGIN

Query Match 36.4%; Score 583.2; DB 9; Length 669;
Best Local Similarity 99.5%; Pred. No. 1.1e-102;
Matches 585; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1015 ttctcatcacctgacgttgttccagaagcgtttcagatggcgcattttgttgagaca 1074
Db 669 TTCTTCATACACCTGACGTTGTTCAGAACGCGTTTCAGATGGCGCATTTGTGTGAGACA 610
OY 1075 gtggcaccgcccgttgaagaatgctaccacaacgcagatcgggtcagcatcatgaag 1134
Db 609 GTGGCACGCGCCGCTTGAAGAAATGCTACACACGACATCGGGCTGAGCATCATGAAG 550
OY 1135 gtggtgtgtggtgtagctctccagttcctctgcagctatatgaccttccccctcagcg 1194
Db 549 GTGTCGTGGGGCTAGCTCTCCAGTCTCTGCAAGCTATATGACCTTCCCTCTACGCG 490
OY 1195 ctgcgtcacacagatggatcaacatgaagaggttcattctgcagcagcagcagctlocaag 1254
|||||

Db 489 CTCGTACACAGATGGATCAAAATGAAGAGGTCATCTTCGACGAGCAGACGTCCAAG 430
QY 1255 gcgctcaaccaactgcyggaacagcgccaagagagaagaatccgagacagacatg 1314
Db 429 GCGCTACCACTGCGGGAACGCGCCAAAGAGAAGAAGAACTCCGAGACACGACATG 370
QY 1315 ctgatggtcagatgatcgcggaagcaacaccgagccgaggtcgtcgccgatgcccagc 1374
Db 369 CTGATGGCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGCCGATGCCGAGC 310
QY 1375 cggggtcattcaaccgtgcacctgtcttcaacaaggcattggggtggtcggaacaccccaag 1434
Db 309 CGGGGCTCATCAACCCGTGCACCTGCTTCACAAGGGCATGGGGGGTCCGACGACCCCCAG 250
QY 1435 agcgcgcccaacctcgccaagaccagcaggaggtagggacatgtaccgggtgtgtg 1494
Db 249 AGCGGCCCACTCTCGCCAAGGACCAGCAGAGGCTAGGGACATGTACCCGGTTGTGTG 190
QY 1495 gcgcaccccggtgcacagactaatcctaacgacagagagaggtccgctcgtcgtcgcc 1554
Db 189 GCGACCCCGGTGCACAGACTAAATCTTAAAGACAGAGAGAGGTCCGCTCATCATCGGCC 130
QY 1555 ctggaagccgacatccccagtgcaagattttccttcagccagggatga 1602
Db 129 CTGAAGCCGACATCCCGACGTGAGATTCTTCTTCAGCCAGGGATGA 82

RESULT 3
AV835197 605 bp mRNA linear EST 22-JUN-2001
LOCUS AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION spontaneous top three leaves adult, heading stage Hordeum vulgare
subsp. spontaneous cDNA clone bah26013, mRNA sequence.
ACCESSION AV835197
VERSION AV835197.1 GI:14527286
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 605)
AUTHORS Sato, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)
COMMENT Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp/
URL: http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct
submission;
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES

Source
1. 605
/organism="Hordeum vulgare subsp. spontaneum"
/cultivar="H602"
/db_xref="taxon:77009"
/clone="bah26013"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. spontaneum top three leaves adult, heading
stage"
/issue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 131 a 188 c 163 g 122 t 1 others
ORIGIN

Query Match 36.3%; Score 581; DB 9; Length 605;
Best Local Similarity 99.8%; Pred. NO. 3e-102;
Matches 592; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 214 ctgctccatcatcgltcaacgaag-accocatcatcgccaagatatgcatctccgagatgc 272
Db 13 CTGCTCTCATCTGTCACGCAAGNACCCTCATCATCGCAAGATATGCATCTCCGAGATGC 72
QY 273 cgcgcacgtcatgttgcccttcaagcgcgcgcacccgagggccgcgaagcccgacgtacgt 332
Db 73 CCGCGACGTGATGTGGCCCTTGCAAGCGCGGCACCGAGGCGCAAGCCAGCAAGTACGT 132
QY 333 tgactactgccccggaagggcaaggttgcgtcatgttccacgggcagcttgcaaccagtgc 392
Db 133 TGACTACTGCCCGGAGGGCAAGGTGGCGCTCATGTCCACGGGCGAGCTTGACCACTGCA 192
QY 393 cgtcttcattcttctgtgtcgtggtcttccatgttaccctaacgcgtcatcacatagctct 452
Db 193 CGTCTTCATCTTCTGCTCGCGGTCTTCCATGTCAACCTACAGCGTCAACCATAGCTCT 252
QY 453 aagccggtctcaaaatgagaacatggaagaatggtgagacagagaccacctccttgaata 512
Db 253 AAGCGGTCTCAAAATGAGAACATGGAAGAATGGAGACAGAGACCACTCCTTGAAATTA 312
QY 513 ccagttcgcaaatgatctctgcacggttccggttccacgcaccaaagcgtctgtgaagcg 572
Db 313 CCAGTTGCAAAATGATCTCTGACGGGTTCGGTTACCGCAGACGACGTCGTCTGTAAGCG 372
QY 573 ccacctggccctctccagcacccttggcatcagatggtgtgtgccttctcaggcagtt 632
Db 373 CCACCTGGGCCCTCTCCAGCACCCCTGGCATCAGATGGGTGGTGGCTTCTTCAGGCAAGTT 432
QY 633 ctcaaggtcagtcaccaaggttgaactacctgaaccttgaagggcaagcttcatcaacgcga 692
Db 433 CTTCAGGTGAGTCCACCAAGGTGAGTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCA 492
QY 693 ttgtgcgaaaacagcaagttcgacttccacaagtatcatcaagaggtcgtatgagagca 752
Db 493 TTTGTGCGCAAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTGATGAGAGACGA 552
QY 753 ctccaaggtcgtctgcgcacatcagcctcccgtctgtggtgtgtgcgcatccta 805
Db 553 CTTCAGGTGCTGCTGTCGGCATCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCA 605

RESULT 4
BE558835 798 bp mRNA linear EST 23-OCT-2001
LOCUS BE558835
DEFINITION HV_CEBD0020I08f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEBD0020I08f, mRNA sequence.
ACCESSION BE558835
VERSION BE558835.3 GI:16336267
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 798)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi
, D.W., Renton, R.D., Oates, R. and Main, D.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT On Aug 14, 2000 this sequence version replaced gi:13266126.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 458
Seq primer: AATTAAACCTCACTAAAGCG

Db	193	CACACTCACCTGGGGTGTGATCATCATCCCTCTCATCATCCTCTGTGTGTGGAAACCAAGC	252
QY	893	tggagatgatcatcatatggagatygccctggagatccaggaccggygcagcgtcatcaag	952
Db	253	TAGAGATGATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGTGAGCGGTATCAAGG	312
QY	953	gggccccgtgtgtcagccccagcaacaagttctctgttccaccgccccgactggtcc	1012
Db	313	GGGCACCCGTGTGTGAGCCCAACAAGTCTTCTGTGTCCACCGCCCGACTGGGTCC	372
QY	1013	tctcttcatacacctgtgaagtgttccagaaacggttcagatgycgcatlttgttga	1072
Db	373	TCTTCTTCATACACCTGACCTGTGTCCAGAACGCGTTTCAGATGGCACATTTGCTGTGA	432
QY	1073	caatgycacagccccggttgaagaatgtctaccacaagcagatcgygctgagcatcatga	1132
Db	433	CAGTGGCCACGCCCCGGCTTGAAGGACTGCTTCATATGAACATCGGGCTGAGCATATGA	492
QY	1133	aggtgtgtgtggtgctaagctctccagttcctctgcagctatatgacctccccctacg	1192
Db	493	AGGTGCTGTGGGGCTGGCTCTCCAGTCTGTGCAGTACATCAACCTTCCCCCTTACG	552
QY	1193	cgctcgtcacacagatggtatcaaacatgaagaggtcactcttcagacgagcagtcgca	1252
Db	553	CGCTAGTCACACAGATGGGATCAACATGAGAAGGTCCACTTCGACGAGCAGACAGCCA	612
QY	1253	a 1253	
Db	613	A 613	

RESULT	6	
BE405266		
LOCUS		
DEFINITION		536 bp mRNA linear EST 21-JUL-2000
ACCESSION	BE405266	WHE1210_E11_I22S Wheat etiolated seedling root cDNA library
VERSION	BE405266	Triticum aestivum cDNA clone WHE1210_E11_I22, mRNA sequence.
KEYWORDS	BE405266.1	GI:9364734
SOURCE		EST.
ORGANISM		bread wheat.
REFERENCE		Triticum aestivum
AUTHORS		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Triticum.
TITLE		1 (bases 1 to 536)
JOURNAL		Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
COMMENT		The structure and function of the expressed portion of the wheat genomes
		Unpublished (2000)
		Contact: Olin Anderson
		US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
		800 Buchanan Street, Albany, CA 94710, USA
		Tel: 5105595773
		Fax: 5105595818
		Email: candersn@pw.usda.gov
		Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
		Seq primer: Strategene SK primer.

FEATURES
source

```

/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1210_E11_I22"
/clone_lib="Wheat etiolated seedling root cDNA library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli SOLR"
note="Vector: Lambda Uni-ZAP XR, excised phagemid;

```

Site_1: EcORI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Query Match	25.1%;	Score 402.2;	DB 10;	Length 536;
Best Local Similarity	87.9%;	Pred. No. 8.9e-68;		
Matches 474;	Conservative	0;	Mismatches 58;	Indels 7;
				Gaps 3;

[illegible]

JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shln-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshln@genes.nig.ac.jp.
Location/Qualifiers
source 1. .402
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
/db_xref="taxon:77009"
/clone="bah27901"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 60 a 116 c 127 g 96 t 3 others
ORIGIN
Query Match 24.7%; Score 395.8; DB 9; Length 402;
Best Local Similarity 98.8%; Pred. No. 1.4e-66;
Matches 397; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1148 tagctctccagttcctctgcaagctatatagacctcccccttaagcgctgcacacaga 1207
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Db 402 TAGCTCTCCAGTCTCNTNTGCAGCTATATGACCTTCCCCCTNTACGCGCTGTCACACAGA 343
QY 1208 tgggatcaacatgaaagaggttcacatcttcgacgacgacagcgtccaagcgctcccaact 1267
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Db 342 TGGGATCAACATGAGAGGTCCATCTTCGACGACGACAGCGTCCAAGGCGCTCACCAACT 283
QY 1268 ggcggaacacgycgaagagaagaagaagtcgccgagacacgacatgctgagctcaga 1327
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Db 282 GCGCGAACACGCGCAAGGAGAAGAAAGTCCGAGACACGACATGCTGATGGCTCAGA 223
QY 1328 tgatcgcgacgcaacacgagccgagctcgtcgccgagtccgagccggggtcattcac 1387
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Db 222 TGATCGGCGACGCAACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGCTCATCAC 163
QY 1388 ccgtgcacctgcttcacaagggcatggggcggtcgagacgacccccagagcgccacact 1447
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Db 162 CCGTGCACTGCTTCACAGGGCATGGGGCGGTCCGACGACCCCCAGAGCGGCCCACT 103
QY 1448 cgccaagagaccagcagaggttagggacatgtaccgggtgtgtggtggcgacccggtgc 1507
|||||
Db 102 CGCCAAGGACCCAGCAGAGGCTAGGGACATGTACCCGGTGTGTGTGGCGACCCGGTGC 43
QY 1508 acagactaaatcctaagcagagagaggtccgctcgctcgt 1549
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Db 42 ACAGACTAAATCCTAACGACAGAGAGGTCGCCCTCATCAT 1
RESULT 8
BG904891/c 490 bp mRNA linear EST 05-JUN-2001
LOCUS Talr1135F04F Talr1 Triticum aestivum cDNA clone Talr1135F04 3',
DEFINITION mRNA sequence.
ACCESSION BG904891
VERSION BG904891.1 GI:14312567
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Cloutier,S., Dong,G. and Walsh,A.
TITLE Wheat functional genomics- Thatcher Lr1 cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 135 row: F column: 04
Seq primer: M13 Forward.
Location/Qualifiers
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/organism="Triticum aestivum"
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/clone_lib="Talr1"
/tissue_type="leaf tissue"
/dev_stage="14 Days old"
/lab_host="E. coli XL0R"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector PBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
BASE COUNT 90 a 143 c 130 g 127 t
ORIGIN
Query Match 21.4%; Score 343.2; DB 10; Length 490;
Best Local Similarity 90.6%; Pred. No. 2.1e-56;
Matches 366; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1199 tcacacagatgagatcaaacatgaagaggttcacatcttcgacgacgacagcagtcgaagcgc 1258
|||||
Db 490 TCACACAGATGGGATCAACATGAAAGAGGTTCATCTTCGACGACGACGCGCCAAAGCGGC 431
QY 1259 tcaccaactgycgaacacgycgaagagaagaagaagtcgccgagacacgacatgctga 1318
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Db 430 TGACAAACTGGCGGACACGCGCCAAAGGAGAAGAAGTCCGAGACACGACATGCTGA 371
QY 1319 tggctcagatgacgycgacgcaacaccgagccgagctcgtcgccgagtccgagccggg 1378
|||||
Db 370 TGGCGAGATGATCGCGGACGCGACGCCACGCCAGGGCGTCCGCTCATGCGCGG 311
QY 1379 gctcatcacccgtgaacctgttcacaagggcatggggcggtcgagacacccccaagcgc 1438
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Db 310 GCTCGTGGCAGTGCACCTGCTTCACAAAGGCAATGGGACGCTCCGACGATCCCAAGACA 251
QY 1439 cgcccaacctcgccaagagaccagcagaggttagggacatgtaccgggtgtgtggtgcgc 1498
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Db 250 CGCCAACCTCGCCCAAGGGCCATGGAGGAGGCTAGGGACATGTACCCGGTGTGTGGCGC 191
QY 1499 acccggtgcacagactaaatcctaagcagagagaggtccgctcgtcgctcgccctcg 1558
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Db 190 ATCCAGTGCACAGACTAAATCTGCTGACACGAGAGAGTCCGCTCGTCCGACACTCG 131
QY 1559 aagccgacatccccagatgcatgttctcctcagccaaggtatga 1602
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Db 130 ATGTGACATTCACGACGAGATTCTTCTTCCCTCAGCCAAAGGATGA 87
RESULT 9
BI954631 688 bp mRNA linear EST 19-OCT-2001
LOCUS BI954631
DEFINITION HYSMEm0018P07f Hordeum vulgare green seedling EST library
HYCDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone
HYSMEm0018P07f, mRNA sequence.
ACCESSION BI954631
VERSION BI954631.1 GI:16300302
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae ; Triticeae; Hordeum.

1 (bases 1 to 688)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected Morex (compatible) seedling cDNA library

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 236
Seq primer: AATTACCCCTCACTAAGCG
High quality sequence stop: 501.

FEATURES
source

1. .688
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMem0018P07f"
/clone_1lb="Hordeum vulgare green seedling EST library
HVCDA0014 (Blumeria infected)"
/tissue_type="green seedling leaf"
/lab_host="TJC121"
/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Morex (mla) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were infected with isolate 5874 of
Blumeria graminis f. sp. hordei, and leaves were harvested
24, 48 and 72 hr post-inoculation and snap frozen (Wise).
In the TJ Close lab at the University of California,
Riverside, total RNA was prepared from each sample pool,
equal quantities of all three RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give Bluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 129 a 185 c 258 g 113 t 3 others
ORIGIN

Query Match 17.8%; Score 284.8; DB 10; Length 688;
Best Local Similarity 83.2%; Pred. No. 4.1e-45;
Matches 347; Conservative 0; Mismatches 68; Indels 2; Gaps 2;

Oy 1 atgtcgacaaaaaagggtgctcgcgcgaggagctgccggagagcgcgtctgtggcggtg 60
Db 210 ATGTCGACAAAAAGGGTCCGCGCGGAGAGCTGCCGAGACGCCCTCGTGGCGGTG 269
Oy 61 gcggtgtcttcgcgcgcacatgtgtctgtctcgtcctcatgtgaacagcgctccacaag 120
Db 270 GCGGTGCTCTCGCCGCGCATGTGTGTCTCCTCATGAGACGAGACTCCACAAG 329

Oy 121 ctgcgccattgtctccagcacgcgcacaagaaggccctgtggaggcgcttgagaagatg 180
Db 330 CTCGACATTTGGTTCAGCACCAGGCAAGAAGGCCCTGTGGAGGGCGCTGCACAAATG 389
Oy 181 aagcgagctcatgtctgtgtggttcataccctgtcctcatcgtcgaacagcccc 240
Db 390 AAGCGGAGCTCATGCTGGCGGCTTAATATGCTGCTCCTAAATGCTCACGAGGAACCG 449
Oy 241 atcatcgccaagatatgatctccgaggatgccgcgcagcgtcatgtggccctgcaagcgc 300
Db 450 ATCATCGCCAAATATGATCTCCGAGGATCCCGGACAGCAAGTAGCCCTGCAGGCAC 509
Oy 301 -ggcaccgaggcgccgaagcccgcaagtacgttgaactact-gccccgaggccaagtgg 358
Db 510 GGGCGTGAAGGGCCCCGAGGGCGATGAAGACGTTGACAGCTGGCCGGGGGGCATGGAGG 569
Oy 359 cgtcatgtccaagcgagcgttcgacacagctgcacgctctcatctctcgtgcgcg 415
Db 570 GACCACGGTTAACGACCGNTTAGCCGAGCTACAGCGATATAGTTCAGAGCTAGGGG 626

RESULT 10
BI808093 773 bp mRNA linear EST 02-OCT-2001
LOCUS
DEFINITION C002D08 Oryza sativa mature leaf library induced by M.grisea Oryza
sativa cDNA clone C002D08, mRNA sequence.

ACCESSION BI808093
VERSION BI808093.1 GI:15855281
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 773)
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pel,Y.X., Wu
H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.

TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.

FEATURES
source
1. .773
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="C002D08"
/clone_1lb="Oryza sativa mature leaf library induced by
M.grisea"
/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"

BASE COUNT 178 a 209 c 217 g 169 t
ORIGIN

Query Match 15.8%; Score 253; DB 10; Length 773;
Best Local Similarity 67.3%; Pred. No. 5.7e-39;
Matches 445; Conservative 0; Mismatches 185; Indels 31; Gaps 5;

Oy 838 ctcatcgattcttcatccctctcgtgatcctctgtgtgttgaaaccaagctggag 897
Db 63 CGCACCTTATCTGATTCTGTGTGCCACCTGTCACCTCAGTGTGTGGACAACCTGAG 122
Oy 898 atgatcatcatgagatgagccctggagatccagcagcgggcgagcgltcatcaaggggcc 957
Db 123 ATTGTATCATGAGAG-GCCACAGAGATCCAGAACACGGCACTGTGATCAAGGAGCA 181

[illegible]

RESULT	11
LOCUS	BG904890
DEFINITION	Talr1l35F04R Talr1 Triticum aestivum CDNA clone Talr1l35F04 5', mRNA sequence.
ACCESSION	BG904890
VERSION	BG904890.1
KEYWORDS	GI:14312566
SOURCE	EST.
ORGANISM	bread wheat. Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Triticum. 1 (bases 1 to 518) Cloutier, S., Dong, G. and Walsh, A. Wheat functional genomics- Thatcher Lr1 CDNA library Unpublished (2001) Contact: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fax: (204) 983-4604 Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average inset size is >2.2 kb Plate: 135 row: F column: 04 Seq primer: M13 Reverse.
FEATURES	Location/Qualifiers
SOURCE	1..518 /organism="Triticum aestivum"

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BASE COUNT      100 a
ORIGIN           167 c      160 g      91 t
/cultivar="Tatcher Lr1"
/db_xref="taxon:4565"
/clone="TaLr1135F04"
/clone_lib="TaLr1"
/tissue_type="leaf tissue"
/dev_stage="14 Days old"
/lab_host="E. coli XL0R"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector PBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."

```

Query Match	12.8%;	Score 204.6;	DB 10;	Length 518;
Best Local Similarity	79.3%;	Pred. No. 1.1e-29;		
Matches 256;	Conservative	0;	Mismatches 64;	Indels 3;
				Gaps 1
QY 22	ccggcgcgggagctgcccggagagcgccgctcgtggygcgtggygcgtgtcttcgcgcgcacatg	81		
Db 186	CCAGCGAGGACGCTGCCGGAGACGCCGCTCCTGGGCGGTGGCCCTCGTCTTCGCCGTCATG	245		
QY 82	gtgtctcgtgtccgcttcctcatgtgnaacacgctccacaagctcggccattgttccagcac	141		
Db 246	ATCATCGTGTCCGCTCCTCCTCGAGCAGCGCGCTCCATAAGCTCGGCCATTGGTTCACACAAG	305		
QY 142	cggcacaagaagggccctgttgggagggcgctgtgagaagtgaagtcgagtcattgtctggtg	201		
Db 306	CGGCACAGAAGACGGCGCTGGCGGAGGGCGCTGGAGAAGATCAAGCGGAGGCTCATGTCTGTG	365		
QY 202	ggcttcataatccctgtctcctcatcgtcaacgcaagaccccatcatatcgccaagatatgcatc	261		
Db 366	GGCTTCATCTCGCTGCTGCTCGCCCTGACGCGAGGACCC--CATCTCCGGGATATGCAATC	422		
QY 262	tccgagagatgccgcgcgacgctcatgttggcccttgcaagcgcgccaccgagggcgccaagccc	321		
Db 423	TCCGAGAGGCGCCGACGATCATGCGGCCCTTGCAAGCTGCCCCCTGGCTCCGTCAGAGAC	482		
QY 322	agcaagtaagttgactactgccc	344		
Db 483	AAGTACAAGACTACTACTGCGC	505		

RESULT	12
LOCUS	AV835211
DEFINITION	AV835211 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah27g01, mRNA sequence.
ACCESSION	AV835211
VERSION	AV835211.1
KEYWORDS	GI:14527300
SOURCE	EST.
ORGANISM	Hordeum vulgare subsp. spontaneum. Hordeum vulgare subsp. spontaneum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 408)
REFERENCE	Sato, K.
AUTHORS	Barley EST sequencing project in NIG and Okayama Univ
TITLE	unpublished (2001)
JOURNAL	Contact: Kazuhito Sato
COMMENT	Research Institute for Bioresources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kazsato@rib.okayama-u.ac.jp/barley/ URL: http://www.rlb.okayama-u.ac.jp/barley/ Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission: database: http://www.shigen.nig.ac.jp/barley/Barley.html. Location/Qualifiers
FEATURES	

[illegible]

BASE COUNT	154	a	123	c	132	g	211	t
ORIGIN								
Query Match	12.0%; Score 192.6; DB 10; Length 620;							
Best Local Similarity	58.2%; Pred. No. 2.4e-27;							
Matches 358; Conservative	0; Mismatches 254; Indels 3; Gaps 1;							

QY	354	ggtggcgctcatgltccacgcagcggcagcttgcaaccagctgcacgcttcattcatcttgcgtgcgc	413
Db	1	GGTCTCTCTCATTTCTATTCGACGCACATGCATCAGATAACATCCATTACTTTTGTGGC	60
QY	414	ggtcttcctatgltcacctacagcgtcatcacatagctctaagccgctcctaagttagaac	473
Db	61	GGTCCCTCATGTGATATACAGTGCGTAACACTATGTGGCTGGGAANAACCTAAGAATCGTGG	120
QY	474	atggaagaatatggagagacagagaccaactcctcttgaaataccaagttgcgaatgatcctgc	533
Db	121	CTGGAATGCTGGGAACAAGAGACCAGCAACCCATGACTATAGTTTTCAAATGATCCTTC	180
QY	534	acgggtccggttcacgcaccagacgctcgctcgtlgaagcgcacaactgggcctc---ccag	590
Db	181	AAGATTTAGGCTTACTCATGAGACATCATTTGTCAGAGCACATACTAGTTTCTGACC	240
QY	591	caaccttgcatcagatgggtggtgccttcttcaggcagttcttcagtgcatgtaacca	650
Db	241	TATTCCAATCTTCTTTTACATTTGATGTTTCTTCAGACAATTTTCAAGGTCCGTAATA	300
QY	651	ggtggaactacctgaccttgaggcaggtctcatcaacgcgcatitgtcgcaaaaagcaa	710
Db	301	GTCAGATTACTTGACCTCCGCCAATGGCTTTATCAGTGTTCATTATTTAGCTCCGTGAAGTAA	360
QY	711	gttcgacttcaccaagatfacatcaagaaggtcgatgtagagacagcttcaaggtcgtcg	770
Db	361	ATTTAACCTTCCAAGATATATCAAAAAGTCAATTAGAGATGACTTCAAGGTAGTGTGG	420
QY	771	calcagcctcccgcgtgfggggtgtgycgacatccaccctcttcettgacatcaatgggt	830
Db	421	TGTGAGTCCAGTTTGTGGGGATCATTTGTGTGTTTCTTGCTCCCTAAATGTTAGTGGTG	480
QY	831	tggcagcgtcatctgtagattcttccatccctctcgtgtagatccctctgtgtgtaga	890
Db	481	GCATGCATTGTTTGGGCTTCCCTTAATTCCTTTGATTATCATATATGCTGTGGAACACA	540
QY	891	gctgagatgatcatcatcagtagaatggcccttgagatccaggaacggcgagcgtcatcaa	950
Db	541	GCTTCAGGCGGTGTTGACAAGAATGGCTCTTGACATCTCGAGAGACATGCAGTAGTCCA	600
QY	951	gggggcccccgtgt	965
Db	601	GGGAATCCCTCTTGT	615

RESULT 14				
BI432930	643 bp	mRNA	linear	EST 21-AUG-2001
LOCUS	BI432930	643 bp	mRNA	linear EST 21-AUG-2001
DEFINITION	EST535691 P. infestans-challenged leaf Solanum tuberosum cDNA clone			
	PPCA62 5' sequence, mRNA sequence.			
ACCESSION	BI432930			
VERSION	BI432930.1	GI:15257620		
KEYWORDS	EST.			
SOURCE	potato.			
ORGANISM	Solanum tuberosum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Asterales; euasterids I; Solanales; Solanaceae; Solanum.			
REFERENCE	Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,			
AUTHORS	Bougl,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.			
TITLE	Generation of ESTs from Potato Leaves Challenged with Phytophthora			
JOURNAL	infestans, Compatible Interaction			
COMMENT	Unpublished (2000)			
	Contact: Cathy Ronning			

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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 09:37:07 ; Search time 54.2 Seconds
(without alignments)
7260.238 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcgcgacaaaaggggt.....tttccttcagccagcgatga 1602

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425.2	26.5	1851	4	US-09-183-959-9 Sequence 9, Appli
2	312	19.5	1040	4	US-09-183-959-11 Sequence 11, Appli
3	294.6	18.4	538	4	US-09-183-959-13 Sequence 13, Appli
4	225.4	14.1	1869	4	US-09-350-268-1 Sequence 1, Appli
5	216.6	13.5	1725	4	US-09-183-959-1 Sequence 1, Appli
6	148.8	9.3	1831	4	US-09-183-959-7 Sequence 17, Appli
7	117.2	7.3	705	4	US-09-183-959-17 Sequence 3, Appli
8	83.6	5.2	597	4	US-09-183-959-3 Sequence 18, Appli
9	80.4	5.0	750	4	US-09-183-959-18 Sequence 5, Appli
10	59	3.7	472	4	US-09-183-959-5 Sequence 2, Appli
11	51.2	3.2	1575	1	US-07-988-260B-2 Sequence 37, Appli
12	49.4	3.1	1392	3	US-08-478-097A-37 Sequence 42, Appli
13	47.6	3.0	4451	3	US-07-717-294-42 Sequence 10, Appli
14	47.4	3.0	1004	1	US-07-841-646-10 Sequence 10, Appli
15	47.4	3.0	1004	1	US-08-147-023-10 Sequence 10, Appli
16	47.4	3.0	1004	1	US-08-447-570-10 Sequence 10, Appli
17	47.4	3.0	1004	2	US-08-449-700-10 Sequence 10, Appli
18	47.4	3.0	1004	2	US-08-449-699A-10 Sequence 9, Appli
19	47.4	3.0	1259	1	US-07-764-731B-9 Sequence 14, Appli
20	47.4	3.0	1277	1	US-07-841-646-14 Sequence 14, Appli
21	47.4	3.0	1277	1	US-08-147-023-14 Sequence 14, Appli
22	47.4	3.0	1277	1	US-08-447-570-14 Sequence 14, Appli
23	47.4	3.0	1277	2	US-08-449-700-14 Sequence 14, Appli
24	47.4	3.0	1277	2	US-08-449-699A-14 Sequence 1, Appli
25	47.4	3.0	1295	1	US-08-256-368-1 Sequence 3, Appli
26	47.4	3.0	1448	1	US-07-539-756-3 Sequence 7, Appli
27	47.4	3.0	1448	1	US-08-377-292-7 Sequence 7, Appli

28	47.4	3.0	1448	2	US-07-989-847-5 Sequence 5, Appli
29	47.4	3.0	1448	4	US-08-469-411-5 Sequence 5, Appli
30	47.4	3.0	1505	1	US-07-841-646-12 Sequence 12, Appli
31	47.4	3.0	1505	1	US-08-147-023-12 Sequence 12, Appli
32	47.4	3.0	1505	1	US-08-447-570-12 Sequence 12, Appli
33	47.4	3.0	1505	2	US-08-449-700-12 Sequence 12, Appli
34	47.4	3.0	1505	2	US-08-449-699A-12 Sequence 1, Appli
35	47.4	3.0	1822	1	US-07-841-646-1 Sequence 1, Appli
36	47.4	3.0	1822	1	US-07-901-703-1 Sequence 1, Appli
37	47.4	3.0	1822	1	US-08-147-023-1 Sequence 1, Appli
38	47.4	3.0	1822	1	US-08-206-864-1 Sequence 1, Appli
39	47.4	3.0	1822	1	US-08-278-729A-16 Sequence 16, Appli
40	47.4	3.0	1822	1	US-08-480-528A-3 Sequence 3, Appli
41	47.4	3.0	1822	1	US-08-479-666-3 Sequence 3, Appli
42	47.4	3.0	1822	1	US-08-155-343A-16 Sequence 16, Appli
43	47.4	3.0	1822	1	US-08-406-672-16 Sequence 16, Appli
44	47.4	3.0	1822	1	US-08-643-563A-16 Sequence 16, Appli
45	47.4	3.0	1822	1	US-08-447-570-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-183-959-9
; Sequence 9, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 9
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-9

QY	336	ctactgcgcgagggcaaggtgagctcatgtccacgagcgcttgaccagctgcaagt	395
Db	587	caagtgcgcgaggggaagtgccgtcatctccatcaacgagcgctgcaacagctgcaat	646
QY	396	cttcatctctgtgctgcggtcttcacatgtcaccacagcgatcaccatagctaaag	455
Db	647	cttcatctctcttcctgcgcgtcttcacagctctcctacagcgcaatcaccatgagcgctcg	706
QY	456	ccgtctcaaatagagaacatggaagaatgaggagacagagaccctcttggaatacca	515
Db	707	cagggcacaagatacgtgcatggaagagtgaggagaagaagctgcaggaacagactacga	766
QY	516	gttcgcaaatgatcctgcacggttcctcggttcacgacacagagctgcttgtaagcgca	575
Db	767	gttctacatgacccgacgagcttcaagtlcaccacagagacttcttgtaggcagca	826
QY	576	cctg---ggcctctcagcaccctgcacatcagatggtgtggtccttcttcagcgagt	632
Db	827	tatgaatgtgtgaacaagttccacatcatcttaccatcagcaacttcttcgagcgt	886
QY	633	cttcaggtcagtcaccaaggtgactacctgaccttgaggcgagcgttcatcaacgcga	692

Db 887 ctcaaggtccgtgagcgcaagcagactcgcgcgtgcgccacagcttgtcaacgtcca 946

QY 693 ttgttcgcaaaacagcaagttcgcactccacaaagtacatcaagagtgatgagga 752

Db 947 tctgccccctggcagcaagtttgattccagaagtaacatcaagcgcgtctctgagatga 1006

QY 753 ctccaaggtcgtcgtcgcatcacgctcccgctgtgggtgtgtgagatccctcact 812

Db 1007 ctccaaggtgatcgtgggagatcacgtccctctctgtgggtctctgtctcactct 1066

QY 813 ccttgacacatagtgggttgccacgcctcaatctgattcttctcactccctcgtatcc 872

Db 1067 cctcaacgtcgaatgtgatgacacacatgctctgattctcactatgcgggtgtagat 1126

QY 873 cttgtgtgttgaaaccaagcttgagatgatacatgagatggccctggagatccagga 932

Db 1127 cctgtcgtgtgggaaagagctgcaaggtcatcatctgcgcgatggcatcacatcaag 1186

QY 933 ccgggcgagcgtacatcaaggggggcccccgtgtgtcgagcccaagcaaacagttctgt 992

Db 1187 gcgcacagccgtacatccaaagtgcatcccgatgtgtcaagtcagcgaactcctactt 1246

QY 993 ccacgcgccccgactgggtccctctctcattacatacactgaagttgttccagaacgcgt 1052

Db 1247 cgcacgccccacactcgtgtctctcctcactcaccactcaccctctccagaatggtl 1306

QY 1053 gatggcgcatttgtgtgagcagtggtgcacgcgcggcgttgaagaatgtctacacag 1112

Db 1307 gatcatctactctcctctgattctgtatgtagtgcgcatggaactcgtgtctcaac 1366

QY 1113 gatcgggctgagcatcatgaagtgtgtgtgtgagctcctccagttcctctgcagcta 1172

Db 1367 cgaagagttcgtcttggcacgactctgccttggcgtgtgtgtccagtgctgtcag 1426

QY 1173 tatgacctccccctctacgcgtcgtctacacacagatggatcaacatgaagagttcc 1232

Db 1427 cgtgacgctcccgctgtacgcgtcgtctcctccaaatgggtccacatgaagagtt 1486

QY 1233 ctgcagcagcagacgtccaaagcgcgtcaccaactggcggaacacgcccagaagaa 1290

Db 1487 ctgcagcagcagacgtccaaagcgcgtcaagaactggcgccgcgcgaagaagaa 1544

RESULT 2

US-09-183-959-11

; Sequence 11, Application US/09183959

; Patent No. 6303332

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Taramino, Graziana

; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE

; FILE REFERENCE: BB-1125

; CURRENT APPLICATION NUMBER: US/09/183,959

; CURRENT FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: 60/064,493

; EARLIER FILING DATE: No. 6303332ember 5, 1997

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Microsoft Windows 95

; SEQ ID NO 11

; LENGTH: 1040

; TYPE: DNA

; ORGANISM: Zea mays

US-09-183-959-11

Query Match 19.5%; Score 312; DB 4; Length 1040;

Best Local Similarity 64.4%; Pred. No. 2.8e-60;

Matches 484; Conservative 0; Mismatches 265; Indels 3; Gaps 1;

QY 542 ggttcagcaccagacgtctgttgaaagcgccacctg---ggcctctcagcaccctg 598

||||||| ||| ||||| ||||| ||| || || ||| ||

Db 2 ggttcacccacgagacttcgtttgtgagcgacatatgatatgtctcaacaagttccca 61

QY 599 gcatacagatgggtgtggtccctctctcaggcagttcttcaagtgatccacaagtgag 658

Db 62 catccttctacatcaagcaacttcttccggcaggttcttcaagtgatccagcgggcag 121

QY 659 acctgaccttgaggcgagcgttcacatcaacgcgcatttgtcgcaaaacagcaagttc 718

Db 122 actgcgcgtcgcgcacagcgtttgtcaacgttccatctgtgccccctggcaccaaagt 181

QY 719 tccacaagtacatcaagaggtcgatggaagcagactcaaggtcgtctgcgcacagcc 778

Db 182 tccaaagttacatcaagcgcgtctctggaagcagacttcaaggtgaltcgttggagcac 241

QY 779 tccccgtgtgggtgtgtgagatccctcactccctcttcttgcacatcaatgggttgc 838

Db 242 ctcccttgggtctctgtctcactctcctatctcctcaatgtcaatgtgagtagcac 301

QY 839 tcatctgattcttcttcatccctctcgtgatacctctgtgtgtgttggaaccaagctg 898

Db 302 tgcctctgatactccatcatatgcgggtgtgtatcatcctgtccgttggggagcagct 361

QY 899 tgatcatcatgtgagatggccctgtgagatccaggaccggcgagcgtcatcaaggggcc 958

Db 362 gcatcatctgcgcgatgtgcgatcgacatcacagcagcgccgtgatccagggcatcc 421

QY 959 ccgtgtgtgagcccaagcaacaagttcttctgtgttccacgcgcgcgcactgggtct 1018

Db 422 cgctgtgtcgaagtcaagcgaactcctacttctgtgttgcacgcgcacactctgtct 481

QY 1019 tcatacaccctgacgttgttccagaacgcgttccagatggcgcatttgtgtgacagt 1078

Db 482 tcatccacttcaacccctctccagaatggtcttccagatcatctacttctctgtatct 541

QY 1079 ccacgcgcccgttgaagaatgctacacacagcagatcgggtgagcatcatgaagtg 1138

Db 542 atgagtagggagtgactcgtgttccaacgactccgaagaattcgtcttggcaagct 601

QY 1139 tgggtgggtagctctcctcagttcctctgcagctatatgaccttccccctctacgcgt 1198

Db 602 gccttgggtgtgtgttcaggtgtgtgtgcagctacgtgacgtccctctgtacgcgt 661

QY 1199 tcacacagatggatccaacatgaagagttccatcttcgacgagcagacgtccaagg 1258

Db 662 tctccagatgggttccacatgaagcagttccatcttcgacgagcagacccccaagg 721

QY 1259 tcaccaactggcgggaacacgcccgaaggaag 1290

Db 722 tcaagaactggcggccgcgcgaagaagaag 753

RESULT 3

US-09-183-959-13

; Sequence 13, Application US/09183959

; Patent No. 6303332

; GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Rafalski, J. Antoni

; APPLICANT: Taramino, Graziana

; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE

; FILE REFERENCE: BB-1125

; CURRENT APPLICATION NUMBER: US/09/183,959

; CURRENT FILING DATE: 1998-11-02

; EARLIER APPLICATION NUMBER: 60/064,493

; EARLIER FILING DATE: No. 6303332ember 5, 1997

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Microsoft Windows 95

; SEQ ID NO 13

; LENGTH: 538

; TYPE: DNA

; ORGANISM: Zea mays

FEATURE:

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; NAME/KEY: unsure
; LOCATION: (479)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (492)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (499)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (518)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (530)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (537)
; US-09-183-959-13
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Query Match 18.4%; Score 294.6; DB 4; Length 538;
Best Local Similarity 76.0%; Pred. No. 1.7e-56;
Matches 376; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

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QY 964 gtcgagcccaacacaaagtctctctgtgtccaccgccccgactgggtcctctctcata 1023
Db 1 gtgagccaagtgcacaggtctctctgtgttaaccgccccgtgctgtcctctctc 60
QY 1024 cactgacgttgttccagaacgcgttccagatggcgcatlgtgtgacagtggccag 1083
Db 61 cactcaagctcttccagaacgccttccagatggcgcatlgtgtgacagtggccag 120
QY 1084 cccggttgaagaataatgtaccacacgcagatcgggtgagcatatgaagtgtgtg 1143
Db 121 ccagacctgaagaataatgtaccacacgcagatcgggtgagcatatgaagtgtgtg 180
QY 1144 gggctagctctccagttcctctgtcagctatatgacctccccctctacgcgtcgtaca 1203
Db 181 gggctgttctccagttcctctgtcagctatatgacctccccctctacgcgtcgtaca 240
QY 1204 cagatgggatacaaatgaagagttcctctcgaagcagacgtccaaaggcgctcacc 1263
Db 241 cagatggggtgcacatgaagaagacatcttcgagagcagacagcgaaggcggtatg 300
QY 1264 aactggcggaacacggccaaggagagaagaagtccgagacag---gacatgtgatg 1320
Db 301 aagtggcggaacacggccaaggagataaggtgcggcagcggaaggcggaagcttcctgcac 360
QY 1321 gctcagatgctcgcgacgcacaaccgagccggaaggctcgtccgcatgcccgaagccggggc 1380
Db 361 gtgctgagagcgcggaacacacggccaaggccgagccgagcgtcgcgagccggggc 420
QY 1381 tcatacccggtgcacctgtctcacaaggcgatggggcgtcgcgacaccccccagagcg 1440
Db 421 aactgcggtgtcacctgtctcacaagaagtcaggggaggtcgcggaacccgagggng 480
QY 1441 cccacctgcgaag 1455
Db 481 ccggcgctcgnggg 495
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RESULT 4
US-09-350-268-1
; Sequence 1, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
; FILE REFERENCE: 5718-42A-- M103
; CURRENT APPLICATION NUMBER: US/09/350,268
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: M103
; US-09-350-268-1
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Query Match 14.1%; Score 225.4; DB 4; Length 1869;
Best Local Similarity 52.5%; Pred. No. 4.2e-41;
Matches 702; Conservative 0; Mismatches 546; Indels 89; Gaps 6;

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QY 24 ggcgcgggagctgcgcgagagaccgtcgtggcggtggcggtgtcttcgcgcgaatgt 83
Db 92 ggagggcgaagctgagagacacgcctaagtcgtgacgtgtggcgtgtgtctccgtcatcgt 151
QY 84 gctcgtgtccgtctcctcatggaacacggcctccacaagctcggccattgttccagacag 143
Db 152 cctcatcctctcgtctcctcgcgcgcgtccaccacctcggcaaggcactggagcgccg 211
QY 144 gcacaagaaggccctgtggagggcgctggagaagatgaagcgagctcatgtgtgg 203
Db 212 g---aggaagacctgtacagagcgctgtctaagctcaagaagaagctcatgtgtgg 268
QY 204 ctcatatccctgtcctcctcatcgtcaacgaggaaccccatcgcgaagatatgcatctc 263
Db 269 ctctgtctcgtctcctcctcgtcgtctccagga---cttgatacagaagatctgcatcga 325
QY 264 cgaggaagccgcgcgacgtcatgtgcccctgcaagcgcgccagagggcgcaagccag 323
Db 326 cgacagcctcatgtgagcactgtgacgtgcgggtgtgcagcgcaacgcctcgtccta 385
QY 324 caagtacgtgactactgcccgg----- 346
Db 386 ttacgtgtctcctcctcctcctcctccgcggtcgtgtggcgagagatgtcaca 445
QY 347 -----agggcaaggtggcgctcatgtccac 371
Db 446 aggcgcgggggagcttccggcactgttcaagcaagggaagatcccgltgtatcact 505
QY 372 gggcagcttgacacagctgcagcttctcatctctgtcgtcggcgtcttccatgtcaccta 431
Db 506 tcacgccttggagcaggtacacatlttcaatcttgcctlagctatcaacgcgaagtcgtct 565
QY 432 cagcgtcatcaacatagctctaagccgctcacaatatgagaacatggaatggag-a 490
Db 566 cagcgtcgcaacgcgtcctcctgtgagactctgcagatgagatgagatgcactggagaa 625
QY 491 cagagaccactccttgaataaccagttcgcgaatatgatcctgcagcgttccggttcaagc 550
Db 626 caccattcagcaagaaggcgagctctgtccccaagatgatcgccgtytgcaagaatcag 685
QY 551 accagagctcgtctgtgaagcgcaacctgggctctccagcacccttggcatcagatgg 610
Db 686 gttcatccaggaagc---gtgtaagggtacgagaagggcgccgtgttaataatggc 741
QY 611 tgggtgcctctctcagggcagttcttcaagttcagttcaccacaaggttgacttgacctga 670
Db 742 tgcgtcttcttccaacaagttctacagatcagttgtccaacgacgactacattgcatga 801
QY 671 gggcaggttcatcaacgcgcatttgtcgcaaaaacagcaaggttcgacttccacaagtaca 730
Db 802 gactcggttgcataatgagcactttagggggcaccaccaagtttcaactttagcactaca 861
QY 731 tcaagagtgatgaggaagcagacttcaaggtgcgtcgtcgcacatcagcctcccgctgtgg 790
Db 862 tgatcaagctctcgaagaagatttcaagcgagtagtataaagtattactgga 921
QY 791 gtgtgcgactcctcaacccctctccttgacatcaatgggggttgagcagctcatctgat 850
Db 922 ttgtgtgatgactcttctgtcgtcctaagttgcacggggtggcacttctactctgtgatct 981
```

[illegible]

```

RESULT      5
US-09-183-959-1
; Sequence 1, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-1

```

Query Match	13.5%;	Score 216.6;	DB 4;	Length 1725;
Best Local Similarity	51.4%;	Pred. No. 3.6e-39;		
Matches 692;	Conservative	0;	Mismatches 574;	Indels 81;
				Gaps 5;

[illegible]

QY	204	cttcataatccctgtctccctcatcgtcacaaggaaccccatcatcgccaagatatgcatctc	263
Db	200	gttcaatccctcctgtctgtcagcgtgttccaagg---ggatgatccggaggaagcgtgcatccc	256
QY	264	cgagatgcgcgcgacgctcatgtgsccttgcga-----	296
Db	257	tgaacgcctgacattccacatgtctgcacgtcgagaaagccagatgagaagcgcgtgaggc	316
QY	297	-----gcgcggcaaccgagggccgaagcccaagtaacgttgaactactgc---	342
Db	317	cgccaccatgtgagcattttgttagggagcgttgcagagatcgttaggcgtctgtttgcagga	376
QY	343	-----ccggagggcaaggtgscgtcatgttccacggg	374
Db	377	aggcactgcttgggctgagcaatgcccagaagaaggaaaagttccactttgtcccttga	436
QY	375	caagcttgcaaccagctgcacgcttctcatctctgtgtccgcggttctccatgtcacactacag	434
Db	437	agccatacatcagctgcacatttccataattgttctcgtgccaatcacacatgttatttcag	496
QY	435	cgtcatcaccaatagctctaaagcgtctcaaaatgagaacatggaagaatgaggagacaga	494
Db	497	cgtcacacaactatgcttttagaggtgcacagatataccaaccaatggaacaagtgaggaaatgy	556
QY	495	gaccacctccttggataataccagtttcgaaatgatccttgcacggttccggttcaagcacca	554
Db	557	aatta-----aaaagatgctccttggaaatgaggcctaagtgtaaccaaatgtacatcata	610
QY	555	gacgtcgttctgtgaagcgccaccttgggcctctccagcaccccttggca--tcaagatgggt	611
Db	611	tgaatttatcaagaacgctttaagggatattgccaagaattctataatatgagtgtgc	670
QY	612	ggtgsccttcttcaggcagttcttcaggttcagttacccaaggtgagactaccctgacctttag	671
Db	671	gcattccttttgtagcagcttttatagatcagtatcttaatacagattacaccacaatgcg	730
QY	672	ggcaggtctcatcaacgcgcgcatttgttcgcaaaaacagcaagttcgacttccacaagtaacat	731
Db	731	tcttggtttatcatgactcactgccttggaatcccaaaattgttatccatagataacat	790
QY	732	caagaggtcgaatgtagagagcaacttcaaggtcgtctgcgcacatcagcctcccgctgtgggg	791
Db	791	ggtaagggttttagagggcggaattttaagaaagttgtaggcataagctgtgtacttgttgggt	850
QY	792	tgtggcgatccctcaaccctcttcctttgacatcaatggtgttggcacgcctcatcttgatttc	851
Db	851	cttcgtgtgataattctgttgcgtgaatgttaatgctgcgcacacataacttttgattgc	910
QY	852	tttcatccctcctcgtgatccctctcttgtgttggaaccaagctgtagatcatcatgga	911
Db	911	tttccctcccttattcttctgttagccaatttgcactaagctgtagcatgtcatagctca	970
QY	912	gatggcccttgagatccaggaacgggcgagcgtcatcaagggggcccccgtygtcgagcc	971
Db	971	gtagcccatgtagttagctgaggaagcacacagcgttcgagggcgatgtgactcgttaaaacc	1030
QY	972	cagcaacaagttcttctgtgttccaacgcccccgactggtctcctcttccatacaacctgac	1031
Db	1031	atcagatgaacaccttctggttcggaagcctaggggtlataccttaccctgataccactcat	1090
QY	1032	gttgttccagaacgcgtttcagatggcgcatatttgttggacagttggccaagcccgctt	1091
Db	1091	cctctttcagaatgcgtttgagatgggttttcttctgtgatactgagcacttaatgatt	1150
QY	1092	gaagaatagtctaaccaacgcgagatcgggctgagcatcatgaaggtgtgtgtggggtagc	1151
Db	1151	cgactcgtgcatcatatgggacaagttcgtttattgttgccaagcctgtcatcgggggtgt	1210
QY	1152	tctccagttcctctgcagctatatgaccttccccctctaagcgcctcgtcacacagatggg	1211
Db	1211	tattcagcttctctgcagctacagcacttgcctctgttatgccaattgttaaccceagatggg	1270

[illegible]

[illegible]

```

RESULT      6
US-09-183-959-7
; Sequence 7, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 7
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-7

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Query Match	9.38;	Score 148.8;	DB 4;	Length 1831;
Best Local Similarity	48.08;	Pred. No. 3.4e-24;		
Matches 638; Conservative	0;	Mismatches 632;	Indels 60;	Gaps 5;

QY	16	ggggtgcccggcgcgcggaagctgcgcggaagacgcgcgtctgtggcggtgtgtcttcggcc	75
Db	79	gcgggaagcaggggcggtctgcgtgcgggaagacgcccacactgttccgttgcaccgcgtcaccaagc	138
QY	76	gccatggtgtctcgtgtctccgtccctacatggaacaacgycctccacaagaagctcgccattgtgtc	135
Db	139	ctcatgtctgcgtgcgtctgtcttccctcgtctcgagcgcgtccctctcgcgtctcgccaagtgtgctg	198
QY	136	cagcaccgcgcacaagaagagccctgtgtggagagcgcttggagaagatgaaagcggagctcatg	195
Db	199	cgcacaagcacaagcgggaagcgcatgtctgcgcgcgcgtctcgagaagatccgcgcgaagagctgatg	258
QY	196	ctgtgtggcttcataatccctgtctctccatcgtcaacgcagagaccatcatcgcgaagata	255
Db	259	ctgtcgcggagtcatactcgtctgtctgtctcagcagaagcgcgcttcataatcggagatctgc	318
QY	256	tgcattcccgaggatgcccgcgcgaagctcatgtggccctg---caagcgcggaaccgagggc	312
Db	319	gtgcgcgtccctgcgtcttccaccagcgcttccataatctgtccgagagcgactaccaggac	378
QY	313	cgcaagcccacgaagtaagcttgacta-----	338
Db	379	ctgctgcgcacaacgcgacgcacaaccagacgcgctcgacaagaacatgttcggtggccaa	438
QY	339	-----ctgcccggagggcaaggtgycgctcatgttccacgycgagcttcgaccag	387
Db	439	cggctgcacgctctgttggcgagggcacatgaaccttltgttcgtacgagggcccttgacag	498
QY	388	ctgcacgctcttcatactcttcgtgtcgcgcgtcttccatgttcaacctacacagcgtcatcaccata	447
Db	499	ctgcaccggttctctcttcatacccttgttatccatccatgtgttgtacagtttltgtaacagtg	558
QY	448	gctctaagccgcttcaaaaatgagaacatggaagaatatgggagacagagaccacctccttg	507
Db	559	gttctgtcccatgatcaagatctatagcttggaggaagtgggaaaccttagccaggttccaatt	618

QY	508	gaataccaggttcgcaaatgatctcttcacggttccggtttcacgaccagacgttcgtcgtg	567
Db	619	gctgctgaggaattgaaagctagaggaaccaaggtgatgagaagcgacgtcaaccttgtt	678
QY	568	aagcgccaccttgggcctctccagcaaccttggca-----tcagatgggttgggccttc	621
Db	679	ttaacaatgtcttcatccatgtaggcaaaaaataaataacttatttggatgttggcttt	738
QY	622	ttcaggcagttcttcaagttcagttcaccaagggtgactaactgaacctgagggcaggttc	681
Db	739	ttggctcaatticaagggctccataataaaggtcagactaatttggcactgaggttggcctt	798
QY	682	atcaacgcgcatcttgtcgcaaaacagcaagttcgacttccacaaaglatcalcaagagtcg	741
Db	799	gtca---catatcaacagctaccacatccatalatgacttccataatacatatgtaacgagc	855
QY	742	atgtaggacgacttcaaggtcgtcgtcgatcagcctcccgctgtgtgggtgtgacgac	801
Db	856	atggaagatgattacaatgggactatttgtatcagttggccactttgggcatalcgcatt	915
QY	802	ctcaccccttctccttgacatcaatgggttggcaagctcatctgtgattcttccatccct	861
Db	916	gtctgcataattaatcaatgttcatgtgtatccaataataataattctgtgttccttgtcct	975
QY	862	ctcgtatcctcttgtgtgttggaaaccaagctggagatgatcatcatgtagatggccctg	921
Db	976	gttattctgltgcttctaagtgggtactgaacttcagcacgctcatctgtcagttggccttg	1035
QY	922	gaagatccaggaaccgggcgagcgtcatcaagggggcccccgtgttcgagcccgacaag	981
Db	1036	gaagtcgctga--gcaacagcgccattatgttgcctcaacaacttaactgcgtgatgat	1092
QY	982	ttctctcgtttccaccgccccgactgtgtcctcttcttccatacacctgaacgtgttccag	1041
Db	1093	ctatttggtttgaaagcctcggtactctgtgtggtcttatacagttcatattccattcag	1152
QY	1042	aaacgctttcagatggcgcatcttgtgtgacagttggccaagcccgcttgaagaaatgc	1101
Db	1153	aatgcttttgagcttgcaacattcttatgtctctgttggaaactcagtgcaacaacatgt	1212
QY	1102	taccacacgcagatcgggcttgagcatcatgaaagtggtgtgtgggctagctctccagttc	1161
Db	1213	ttcatgaagcactactacatgtgttgcattcgttgaatttcttggcctcttagttcagttc	1272
QY	1162	ctctgcagctatatagaccttccccctctacgcgtcgttcacacagatggatgcaaacatg	1221
Db	1273	tgtgtcagctacagcacactcccgctgaatgtgatatttctcagatgggtcccaagttc	1332
QY	1222	aagagttccatcttcgacgagcagacgctccaaggcgctcaaccaacttggcgaaacagcc	1281
Db	1333	aagaatatcactgtctcggagaacgtgagggagtcgctccacagcgtgtgtcaagagggtt	1392
QY	1282	aaggaaga 1291	
Db	1393	aaggaacagga 1402	

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RESULT 7
US-09-183-959-17
; Sequence 17, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20

```

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; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 17
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Zea mays
;
US-09-183-959-17

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Query Match	7.38;	Score 117.2;	DB 4;	Length 705;
Best Local Similarity	72.48;	Pred. No. 2.5e-17;		
Matches 152; Conservative	0;	Mismatches 58;	Indels 0;	Gaps 0;

QY	618	cttccttcaggcagttctcttcaggctcagttccacccaaggtgtgactactgacctggaaggcgagg	677
Db	175	ctctctccgcagttctcttcaggctcgttcgtaggcagcgagactactgcgcgtgcgcacag	234
QY	678	cttcactcaacgcgcatttgttcgcaaacacagcaagttcgcacttcacacaagtacatcaagag	737
Db	235	cttcgtccaacgctccatctctgccccctgcagcaagattgatttcagaagaatcacatcaacgcg	294
QY	738	gtcgcattgagagcagcacttcaaggtcgttcgttcgcgcatacagccctcccgctgtgtggtgtgc	797
Db	295	gtctctgtgagagatgacttcaaggtgatcgttcgttggggtatcagttcctcctctgttggcctctgc	354
QY	798	gattcctcacccctcttccttgacatcaatgg	827
Db	355	tcctcatcttcctcttcctcaacgltcaatgg	384

RESULT 8
US-09-183-959-3
: Sequence 3, Application US/09183959

```

: GENERAL INFORMATION:
: APPLICANT: Cahoon, Rebecca E.
: APPLICANT: Miao, Guo-Hua
: APPLICANT: Rafalski, J. Antoni
: APPLICANT: Tarantino, Graziana
: TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
: FILE REFERENCE: BB-1125
: CURRENT APPLICATION NUMBER: US/09/183,959
: CURRENT FILING DATE: 1998-11-02
: EARLIER APPLICATION NUMBER: 60/064,493
: EARLIER FILING DATE: No. 6303332ember 5, 1997
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Microsoft Windows 95
: SEQ ID NO 3

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?	TYPE:	DNA
?	ORGANISM:	Zea mays
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(3)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(475)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(520)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(538)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(540)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(552)
?	FEATURE:	
?	NAME/KEY:	unsure
?	LOCATION:	(559)
?	FEATURE:	
?	NAME/KEY:	unsure

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; LOCATION: (568)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (571)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (583)
;
US-09-183-959-3

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Query Match	5.2%;	Score 83.6;	DB 4;	Length 597;
Best Local Similarity	54.6%;	Pred. No. 6.3e-10;		
Matches 189; Conservative	0;	Mismatches 154;	Indels 3;	Gaps 1;

QY	713	tccgacttcacaagtagatcaagaaggtcgaatgtagagacgaattcaaggtctgcgtcgca	772
Dd	34	ttgatttccacaatacatatgactcgcgtgttgtaatatgatagttaaaagagtgttgta	93
QY	773	tcagcctcccgcgtgttgggtgtggcgatccctcacaccttctccttgaatcatcatgsgttg	832
Dd	94	tcagctgttatctgttggtcttctgtaatcttatctcctgcgtcgtgaataataatgatgyc	153
QY	833	gcacgctcatctgtgattcttcttcaatccctctcgtgatatcctctgtgtgttgyaaccaagc	892
Dd	154	acacataacttctgtgttggtccttctgtcctctatttctgttactatattgttgytccaac	213
QY	893	tggagatgatcatcatatgtagatggcccttgagatccag--gaccgggcgagcgtcatca	949
Dd	214	tagagcacattatcatcactcgtgttgctcaagagcgacgabatcatatcaataataacag	273
QY	950	agggggcccccggtgtgcgagcccaagaacaagtctctctgtgtccaccgccccgactggg	1009
Dd	274	aggaagttccgaaaaataaagccatgcgaaggaaccaatttctgtgttccacaagccctlgactag	333
QY	1010	tcctctcttcatacacacctgacgtgtgttccagaagcggttcagat	1055
Dd	334	tccttcatttgattcatcttcatcctcgttccagaagaattcgttcgagat	379

RESULT 9
US-09-183-959-18
: Sequence 18, Application US/09183959

```

; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183, 959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064, 493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 18
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-18

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Query Match	5.0%;	Score 80.4;	DB 4;	Length 750;
Best Local Similarity	71.9%;	Pred. No. 3.4e-09;		
Matches 105; Conservative	0;	Mismatches 41;	Indels 0;	Gaps 0;

[illegible]

Db 364 ctggagagcacttcaagtgatcgtggygatcagccctcttgtggygcttctgtctc 423
QY 802 ctcacctcttcttgcattgacatcatg 827
Db 424 atcttctattcttccaatgtcatg 449

RESULT 10
US-09-183-959-5
; Sequence 5, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Caloon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tarantino, Graziana
; TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 5
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (164)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (351)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (398)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (414)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (427)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (439)..(440)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (447)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (450)
; US-09-183-959-5

Query Match 3.7%; Score 59; DB 4; Length 472;
Best Local Similarity 58.7%; Pred. No. 0.00016;
Matches 101; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 1145 ggcgtacgtctccagttcctctgtcagctatatgacctccccctctaagcgctcgtaacac 1204
Db 151 ggggtgtattatcancctctctgtcagctacagcaccttgcctctgtatgcaattgtaaccc 210
QY 1205 agatgggatcaaacatgaagaggtccattcttcgacgagcagacgtccaaggcgctcacca 1264
Db 211 agatggggagctgtctacaagaagagatcttcaacgagcatgtgcagcagggcgctcctg 270
QY 1265 actggcggaacacgccaagggagaagaagaagtccgagacagcatgct 1316
Db 271 gctgggctcagaaggtcaagatgaaaaaagggaactgagggagctgcatctgct 322

RESULT 11
US-07-988-260B-2
; Sequence 2, Application US/07988260B
; Patent No. 5482843
; GENERAL INFORMATION:
; APPLICANT: BRZEZINSKI, RYSZARD
; TITLE OF INVENTION: ENZYME OF USE IN CHITOSAN
; TITLE OF INVENTION: HYDROLYSIS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,260B
; FILING DATE: 19921214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/98214/MW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1575 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE: Streptomyces N174
; US-07-988-260B-2

Query Match 3.2%; Score 51.2; DB 1; Length 1575;
Best Local Similarity 47.8%; Pred. No. 0.011;
Matches 149; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 75 cgcgatgtgtcgtgtctcgtctcatgtgaacacgagcctcacaaagctcggcattggt 134
Db 635 CACCAAGGACTGGGCGACCGCGCCAAGACACCGTCTTCAGACGAGGCCAGAACGACGA 694
QY 135 ccagcaaccggcacaaagaagccctgtggygagcgctgtgagaagatgaagcgaggtcat 194
Db 695 GCGCGACCGGGTCTTACTTCGACCCGCGCTCAAGCCAGGCCGAAGGCCGAGCGGCTGCGCGC 754
QY 195 gctgggtggcttcataatccctgtctcctcatcgtcaagcaggaaccccatcatcgccaagt 254
Db 755 GCTGGGCCAGTTGCGCTTACTTACGACGCCATCGTGTATGACGGCCCCGGCAACGACCGGAC 814
QY 255 atgcatctcagagatgcgcgcagcgtcatgttggcccttgaagcgcgacccagggcg 314
Db 815 CAGCTTCGGTGGCATCCGCAAGACCGCCATGAAGAAAGGCCAGACCCCGCCAGGGCGG 874
QY 315 caagcccaagcaagtagttagtacttgcgccgagggcaaggtggcgctcatgttcacgg 374
Db 875 CGAGGAGACCACTACCTACCAACGCCCTTCTTGAGCGCCCGCAAGGCCCGCATGCTACCGA 934
QY 375 cagcttgacca 386
Db 935 GGCCGCGCACGA 946

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RESULT 12
US-08-478-097A-37
; Sequence 37, Application US/08478097A
; Patent No. 6040431
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,097A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1392
; OTHER INFORMATION: /product= "MODIFIED OP-1 DNA"
US-08-478-097A-37

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Query Match	3.1%;	Score 49.4;	DB 3;	Length 1392;
Best Local Similarity	47.6%;	Pred. No. 0.027;		
Matches 146;	Conservative 0;	Mismatches 161;	Indels 0;	Gaps 0;
QY 84	gctcgtgtccgtccctcatgtaacacgacctcacacaagctcgccattgttccagcaccg	143		
Db 695	GCCTGCTTTGACATCACAGCCACCAGCAACCACCTGGGTGTGTCATCCGGCACAACTT	754		
QY 144	gcacaaagaagccctgtgtgagagcgtgtgagaagaatgaagcgcgagctcatgtctgtgg	203		
Db 755	GGGCTCTGAGCTCTCGGTGAGACGCTGGATGGGACAGCATCAACCCCAAGTTGGCGGG	814		
QY 204	cttcataaccctgtctcctcatcgtcaacgcaagaccocatcatcgccaagatatgcattc	263		
Db 815	CCTGATTTGGGGCGGCACGGGCCCAAGAACAGCAGCCCTTCATGTTGGCTTTCTTCAAGGC	874		
QY 264	cgaagatgccgcccgaactcatgtgtgcccctgcaagcgcgcgcaaccgagggccgcaagcccg	323		
Db 875	CACGGAGTTCACCTTCCGCAAGCATCCGGTCCACGGGGAGCAAAACAGCCGACCAAGAACCG	934		
QY 324	caagtaagttgaactactgccccggagagcaaggtgycgctcatgttccacgycgacgttga	383		
Db 935	CTTCAAGACGCCCAAGAACCAAGGAAGCCCTGCGGATGGCCAACAGACCCCGGCGGCGG	994		

QY	384	ccagctg	390
Db	995	CCATATG	1001

```

RESULT 13
US-08-717-294-42/c
Sequence 42, Application US/08717294
Patent No. 6114148
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,294
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/345001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 4451 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-717-294-42

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[illegible]

QY	253	atatgcatctccgagatgccgcgcgacgtcatgtgcccctgcaagcgcgcgcaaccgagggc	312
Db	3802	GTGCTGTTGCCGCGGTAGTCTGCCACCTTCTTGCCGCTAGAGAGTACATGATGATGAAC	3743
QY	313	cgcgaagcccgacaagtacgttgactactgcccgcgagggcaaggtgcgctcatgtccaag	372
Db	3742	TGGCTGATGTACAGCGCTGCAACTCTTGCGGGCGCCCTGGGCTCTTGATGCCGTGAATG	3683
QY	373	ggcagcctlgcaccacagctgcaagctcttcac	402
Db	3682	ATCATGGGGGCCAGCAGGTCCACCTTGATC	3653

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RESULT 14
US-07-841-646-10
Sequence 10, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, HORWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841, 646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913

```

```

? FILING DATE: 22-FEB-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 422,613
? FILING DATE: 17-OCT-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 315,342
? FILING DATE: 23-FEB-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 232,630
? FILING DATE: 15-AUG-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 179,460
? FILING DATE: 08-APR-1988
? ATTORNEY/AGENT INFORMATION:
? NAME: PITCHER, EDMUND R.
? REGISTRATION NUMBER: 27,829
? REFERENCE/DOCKET NUMBER: CRP-001CP6
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617/248-7000
? TELEFAX: 617/248-7100
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1004 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: YES
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..951
? OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
? OTHER INFORMATION: /product= "OP1B"
? OTHER INFORMATION: /note= "OP1B - FUSION"
US-07-841-646-10

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	Query Match	Best Local Similarity	Score	DB 1;	Length	1004;		
	Matches	135; Conservative	0;	Mismatches	146;	Indels	0;	Gaps
QY	84	gctcgtgccgtccctcatatggaacacagcgctccacaagaatcgcgaattglttccagaccg	143					
Db	327	GCCTGCTTTGACATCACAGCCACCAGCAACTGGGTGTCATCCGGCACAACCT	386					
QY	144	gcacaagaaggcccctgtggagcgcttgagagaatatgaagcgagctcatgtgtgtgg	203					
Db	387	GGGCCCTCAGCTCTCGGTGAGACGCTGATGGGCGAGAGCATCAACCCCAAGTGGCGGG	446					
QY	204	cctcataccccctgtcctcctcatcgtcacgcaggaaccccatcatcgcgaagatatgtatctc	263					
Db	447	CCTGATTGGGGCGGCACGGCCCCAGAACAGACGCCCTTCATGTGCTTCTTCCAAGGC	506					
QY	264	cgaggaatgcccgcgcgaactcatgttggcccttgcaagcgcygcacccgagggccgcgaagcccg	323					
Db	507	CACGGAGTTCACCTTCGCGACGATCCGGTTCACGGGGAGAACAACAGCGCAGCCAAGACCG	566					
QY	324	caagtaagttagtaactactgccccggagggccaaggttggcgtca	364					
Db	567	CTCCAAAGACGCCCAAGAACCAAGGAAGCCCTGCGGATGGCCA	607					

RESULT 15
US-08-147-023-10
; Sequence 10, Application US/08147023
; Patent No. 5468845
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.

```

1 TITLE OF INVENTION: OSTEOGENIC DEVICES
2 NUMBER OF SEQUENCES: 33
3 CORRESPONDENCE ADDRESSES:
4 ADDRESSEE: TESTA, HURWITZ & THIBEAULT
5 STREET: 53 STATE STREET
6 CITY: BOSTON
7 STATE: MASSACHUSETTS
8 COUNTRY: U.S.A.
9 ZIP: 02109
10
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: PatentIn Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/147,023
18 FILING DATE: 21-FEB-1992
19 CLASSIFICATION: 530
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 810,560
23 FILING DATE: 20-DEC-1991
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 827,052
26 FILING DATE: 28-JAN-1992
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 660,162
29 FILING DATE: 22-FEB-1991
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 621,988
32 FILING DATE: 04-DEC-1990
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 621,849
35 FILING DATE: 04-DEC-1990
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 616,374
38 FILING DATE: 21-NOV-1990
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 600,024
41 FILING DATE: 18-OCT-1990
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 599,543
44 FILING DATE: 18-OCT-1990
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 579,865
47 FILING DATE: 07-SEP-1990
48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER: US 569,920
50 FILING DATE: 20-AUG-1990
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US 483,913
53 FILING DATE: 22-FEB-1990
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 422,613
56 FILING DATE: 17-OCT-1989
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 315,342
59 FILING DATE: 23-FEB-1989
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: US 232,630
62 FILING DATE: 15-AUG-1988
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: US 179,460
65 FILING DATE: 08-APR-1988
66 ATTORNEY/AGENT INFORMATION:
67 NAME: PITCHER, EDMUND R.
68
69 REGISTRATION NUMBER: 27,829
70 REFERENCE/DOCKET NUMBER: CRP-001CP6
71 TELECOMMUNICATION INFORMATION:
72 TELEPHONE: 617/248-7000
73 TELEFAX: 617/248-7100
74 INFORMATION FOR SEQ ID NO: 10:
75 SEQUENCE CHARACTERISTICS:
76 LENGTH: 1004 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Op1b"
; OTHER INFORMATION: /note= "Op1b - Fusion"
US-08-147-023-10

```

Query Match	3.08%;	Score 47.4;	DB 1;	Length 1004;
Best Local Similarity	48.08%;	pred. No. 0.069;		
Matches 135; Conservative	0;	Mismatches 146;	Indels 0;	Gaps 0;

QY	84	gctcgtgtgccgtcctcatgtaacacgacctccacaagctcggccattgtgtccagcaccg	143
Db	327	gctcgtgtttgacatcacagaccacacacacactgggtgtcaatccgggcacacact	386
QY	144	gcacaagaagggccctgtgtggaagcgctgtgagaagatgaagcgagctcatgtgtg	203
Db	387	ggcgcttcagctctcgggtgagacgcgtggatgggcagagcatcaacccccaagtggcggg	446
QY	204	cttcataccctgtcctcctcatcgttcacgcaggaaccocatcatcgcgaagatgcatctc	263
Db	447	ccctgattggggcggcacggcccccagaacacagcagcccttcattggtggctttccaaggc	506
QY	264	cgaagatgccgcccgaactcatgttgccctgcaagcgcggcacccgagggccgcaagccag	323
Db	507	cacggaggtccactctccgcacgacatccgggtccacggggagcaaacacagccacgaacccg	566
QY	324	caagtaagttagctactactgccccgagagggcaaggtgcgctca	364
Db	567	ctccaagacgcccacaagaaccaggaagcccttcgggatggcca	607

Search completed: July 23, 2002, 11:27:17
Job time: 6610 sec

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; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1004 base pairs

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 10:04:52 ; Search time 214.15 Seconds
(without alignments)
12843.787 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcgacaaaaaagggt.....tttccttcagccagggatga 1602

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1602	100.0	1602	19	AAV35022	Hordeum vulgare cv
2	1600.4	99.9	1917	19	AAV35026	Hordeum vulgare ML
3	1316.8	82.2	1868	20	AAZ30409	Wheat Mlo fungal r
4	1316.8	82.2	1868	22	AAF24583	Nucleotide sequenc
5	1315.2	82.1	1711	21	AAA52715	Wheat Mlo homologu
6	1314.8	82.1	1692	20	AAZ30410	Wheat Mlo fungal r
7	1314.8	82.1	1693	22	AAF24584	Nucleotide sequenc
8	1305.6	81.5	1886	20	AAZ30411	Wheat Mlo fungal r
9	1305.6	81.5	1886	22	AAF24585	Nucleotide sequenc

10	936.8	58.5	1635	19	AAV35030	Hordeum vulgare ML
11	765.6	47.8	1611	19	AAV35028	Oryza sativa MLO g
12	573	35.8	2425	19	AAV35025	Hordeum vulgare ML
13	569.8	35.6	678	21	AAA52707	Wheat Mlo homologu
14	493.4	30.8	563	21	AAA52704	Soybean Mlo homolo
15	425.2	26.5	1815	21	AAZ49564	Maize MLO6 protein
16	425.2	26.5	1851	20	AAZ49564	Maize MLO6 protein
17	379	23.7	2030	21	AAZ49561	Maize MLO2 protein
18	368.6	23.0	845	21	AAZ49560	Maize MLO1 protein
19	329	20.5	2197	20	AAZ30412	Arabidopsis thalia
20	329	20.5	2197	22	AAF24586	Nucleotide sequenc
21	312	19.5	1040	20	AAZ30415	Zea mays SCLBr pro
22	298.8	18.7	1782	20	AAZ30415	Arabidopsis thalia
23	298.8	18.7	1782	22	AAF24589	Nucleotide sequenc
24	294.6	18.4	538	20	AAZ30413	Zea mays SCLBr pro
25	285.8	17.8	1935	20	AAZ30413	Arabidopsis thalia
26	285.8	17.8	1935	22	AAF24587	Nucleotide sequenc
27	285.8	17.8	2148	21	AAZ49560	Arabidopsis thalia
28	272	17.0	4105	19	AAV35029	Hordeum vulgare ML
29	260.6	16.3	1938	21	AAZ50126	Soybean Mlo homolo
30	239.4	14.9	2096	19	AAV35023	Hordeum vulgare ML
31	225.4	14.1	1869	21	AAZ50126	Maize MLO3 cDNA.
32	225.4	14.1	1869	22	AAZ501109	Maize monogenic di
33	219.6	13.7	1666	21	AAZ52718	Wheat Mlo homologu
34	216.6	13.5	1725	20	AAZ58270	Zea mays SCLBr pro
35	216.6	13.5	1798	21	AAZ49566	Maize MLO8 protein
36	214.2	13.4	1496	21	AAZ52708	Wheat Mlo homologu
37	213	13.3	1745	21	AAZ52703	Soybean Mlo homolo
38	198.8	12.4	1811	20	AAZ30414	Arabidopsis thalia
39	198.8	12.4	1811	22	AAF24588	Nucleotide sequenc
40	198.8	12.4	1880	19	AAV35031	Arabidopsis thalia
41	178.6	11.1	1660	21	AAZ49565	Maize MLO7 protein
42	161.2	10.1	513	21	AAZ52702	Rice Mlo homologue
43	161	10.0	960	21	AAZ52713	Soybean Mlo homolo
44	150.4	9.4	1831	20	AAZ58273	Zea mays SCLBr pro
45	148.8	9.3	1841	21	AAZ49562	Maize MLO4 protein

ALIGNMENTS

RESULT 1	
AAV35022	
ID AAV35022	standard; DNA; 1602 BP.
XX AAV35022;	
AC AAV35022;	
XX AAV35022;	
DT 13-OCT-1998	(first entry)
XX 13-OCT-1998	
DE Hordeum vulgare cv. Ingrid MLO gene.	
XX Hordeum vulgare cv. Ingrid MLO gene.	
XX Barley; MLO; mildew; pathogen; resistance; ss.	
KW Barley; MLO; mildew; pathogen; resistance; ss.	
XX Barley; MLO; mildew; pathogen; resistance; ss.	
OS Hordeum vulgare.	
XX Hordeum vulgare.	
FH Key	Location/Qualifiers
FT CDS	1..1602
FT	/*tag= a
FT	/product= MLO protein
XX	
PN W09804586-A2.	
XX W09804586-A2.	
PD 05-FEB-1998.	
XX 05-FEB-1998.	
PF 29-JUL-1997;	97WO-GB02046.
XX 29-JUL-1997;	
XX 07-MAR-1997;	97GB-0004789.
PR 29-JUL-1996;	96GB-0015879.
PR 30-OCT-1996;	96GB-0022626.
XX 30-OCT-1996;	
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.	
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.	
PI Bueschges R, Panstruga R, Schulzelefer PMJ;	

XX WPI: 1998-159149/14.
DR P-PSDB; AAW59442.
XX
PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Claim 2; Fig 2; 150pp; English.
XX
CC The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of Mlo function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
SQ Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;

Query Match 100.0%; Score 1602; DB 19; Length 1602;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 atgtcgcacaaaaaagggtgtccgycgcggagagtcyccggagacgcgcgtctggcggtg 60
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RESULT 2
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ID AAV35026 standard; cDNA; 1917 BP.
XX
AC AAV35026;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.

XX OS Hordeum vulgare.
XX FH Key Location/Qualifiers
FT CDS 225..1826
FT /*tag= a
FT /product= MLO protein
FT 1890..1895
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XX PN WO9804586-A2.
XX PD 05-FEB-1998.
XX PF 29-JUL-1997; 97WO-GB02046.
XX PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX Bueschges R, Panstruga R, Schulzelefert PMJ;
XX WPI; 1998-159149/14.
DR P-PSDB; AAW59443.
XX
PT New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 7; 150pp; English.
XX
CC The sequence is that of the MLO gene, wild-type MLO exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of MLO function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
SQ Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

Query Match 99.9%; Score 1600.4; DB 19; Length 1917;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1601; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	1725	ccggtgcacagactaatcctaacgacagagagaggtccgcctcgtcgcgcctcgaa	90.3%	1784	1868	0	0
QY	DB	1561 gccgacatccccagtcagattttcctcaccagggatga 1602		1826	1868	0	0
DB	1785	gccgacatccccagtcagattttcctcaccagggatga 1826		1826	1868	0	0
<p>RESULT 3</p> <p>AAZ30409 standard; DNA; 1868 BP.</p> <p>AAZ30409; 21-DEC-1999 (first entry)</p> <p>Wheat Mlo fungal resistance gene TrmLol.</p> <p>Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition; papilla; contact site; callose; carbohydrate; phenol; transgenic plant; Mlo; Erysiphe graminis; powdery mildew; ss.</p> <p>Triticum sp.</p> <p>Location/Qualifiers</p> <p>176..1780</p> <p>/*tag= a</p> <p>/product= "fungal resistance protein Mlo1"</p> <p>WO9947552-A2.</p> <p>23-SEP-1999.</p> <p>17-MAR-1999; 99WO-EP01779.</p> <p>17-MAR-1998; 98US-0042763.</p> <p>(NOVS) NOVARTIS AG.</p> <p>(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.</p> <p>Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;</p> <p>WPI; 1999-571820/48.</p> <p>P-PSDB; AAY26966.</p> <p>New proteins useful for generating transgenic plants resistant to fungal infection -</p> <p>Claim 2; Page 58-60; 102pp; English.</p> <p>This sequence represents the coding region for the wheat fungal resistance gene TrmLol. The Mlo protein confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mlo sequences are used to generate transgenic plants resistant to fungal pathogens, especially Erysiphe graminis (powdery mildew).</p> <p>Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other;</p>							
QY	DB	22 ccgagcgagagctgccgagagagccgtcgtggcggtgagcggtgtcttcgagccatg		81	1868	6	2

D	b	200	ccagcgaggaacgctgcgcgagacgcgcctctctggcggtgccccctcgtctctcgcgcgtcatg	259
Q	y	82	gtgcctcgtgtccgctccctcatggaacacggcctccacaagctcggccattggttccagcac	141
D	b	260	atcatcgtgtccgtctccctcctctgagacacgcgcctccataagctcggccattggttccacaag	319
Q	y	142	cggcacaagaagcgccctgttggagcgcgcttgagagaagatgaaagcggaagctcatgtctgtg	201
D	b	320	cggcacaagaacgcgcgttgcgagagcgcttgagagaagatcaagcggaagctcatgtctgtg	379
Q	y	202	ggcttcataaccctcgtctccctcatcgtcacgcggaaccccatcatcgccaagatatgcac	261
D	b	380	ggcttcataccctcgtcgtctcgcgcgtgacgcgagagacc--catctcggagatatgcac	436
Q	y	262	tccgagatgcgcgcgcgacgctcatgttggcccttgcaagcgcgacacgagggcgcgcaagcc	321
D	b	437	tccgagaaagcgccgcgacgacatcatgcgcccttgcaagctgccccctgctccgtccaagagc	496
Q	y	322	agcaagtaagttgactactgccc--ggaaggccaagttggcgctcatgttccacggygcgc	378
D	b	497	aagtaacaagaactactactcgtcgccaacaacagggccaaggtgtcgtcatgttccacggygcgc	556
Q	y	379	ttgcaaccagctgcacgctctcatctctcgtgtcgcgcggtcttccatgtccactacagctc	438
D	b	557	ttgcaaccagctgcacacatatcatctcgtgtcgcgcgtcttccatgtlcaactacagcgtc	616
Q	y	439	atcaccatagctctcaagccgtctcaaatatgagaacatltggaagaaltggygagacagagacc	498
D	b	617	atcatcatgctctcaagccgtctcaaatatgagaaccttgaagaalaatggygagacagagacc	676
Q	y	499	accctccttggaaataccaggttcgcaaatatgatccctgcacggttcccggttcaacgcaaccagc	558
D	b	677	gcctcccttggaaataccaggttcgcaaatatgatccctgcgcggttcccggttcaacgcaaccagc	736
Q	y	559	tcggtcgtgaaagcgcaacccttgggctctctccagcaaccccttgcacatcagatgggtgtgccc	618
D	b	737	tcggtcgtgaaagcgcaacccttgggctctctccagcaaccccggtcagatgggtgtgccc	796
Q	y	619	ttcttcaggcagttcttcaaggtcagtcacccaaggttgactacccttgagggcaggc	678
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Q	y	679	ttcatcaacgcgcatttgtcgcgaacaaacagcaagttcgcacttccacaagtlacatcaagag	738
D	b	857	ttcatcaacgcgcatttgtcgcgaacaaacagcaagttcgcacttccacaagtlacatcaagag	916
Q	y	739	tcgatggaggaagcacttcaaggtcgtcgtcgcatcacgcctcccgctgtggggtgtggcg	798
D	b	917	tcgatggaggaagcacttcaaggtcgtcgtcgcatcacgcctcccgctgtgtgtgtggcg	976
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D	b	1097	ctggagatccaggaacgcgggcgagcgttcatcaagggggcccccgctgttgcagcccaagcaac	1156
Q	y	979	aagttcttctgttccacacgcccccgactgggtccctcttcatatacacctgacgctattc	1038
D	b	1157	aagttcttctgttccacacgcccccgactgggtccctcttcatatacacctgacgctattc	1216
Q	y	1039	cagaacgcggttccagatggcgcatattgtgtgagacagltggccaacgccccggttgaagaaa	1098
D	b	1217	cagaacgcggttccagatggcacattcgtgtgagacagltggccaacgccccggttgaagaaa	1276
Q	y	1099	tgtctaacacacgcagatcgggctgagcatcatgaaggtgtgtgtgggtagctctccag	1158
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QY	1159	ttcctctgcagctatatatgaccttccccctctacgcgctcgttcacacagatggtgataaac	1218
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QY	1219	atgaagaaggtccatctctgcacgagcagacggtccaaggcgtcaaccaactgycggaacacg	1278
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QY	1279	gccaaagagaagaagaagaagtcgcgagacacgcgacatgctgatggtcagatgatacgcgcac	1338
Db	1457	gccaaagagaagaagaagaagtcgcgagacacgcgacatgctgatggtcagatgatacgcgcac	1516
QY	1339	gcacaacgcgagccgaggtctgctgcgcgatatgcgagccggggtcatcacccgtgcacctg	1398
Db	1517	gcgacgcccaagccgaggggctgcgcccatgtcctagccggggtctgctgcacagtgcacctg	1576
QY	1399	cttcacaaggcgcatgtggcggtctgcgacgaccccccaagcgcgcgccacctcgcgccaagacc	1458
Db	1577	cttcacaaggcgcatgtggcggtctgcgacgaccccccaagcgcgcgccacctcgcgccaagacc	1636
QY	1459	cagcagagaggtctagggacatgtacccggttgtgtgtgcgcgaccccggtgcacagactaat	1518
Db	1637	atggaaggaaggtctagggacatgtacccggttgtgtgtgcgcgacccagtgcacagactaat	1696
QY	1519	cctaaacgacaggaaggaagtcgcgcctcgtctgcgcgcctcgaagccgacatccccagtgca	1578
Db	1697	cctgcgtgacaggaaggaaggtcgtctcgtctgcgcgacactgcatgtgcacatccccagcgca	1756
QY	1579	gatttttccttcagccagggatga	1602
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RESULT	4
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ID	AAAF24583 standard; DNA; 1868 BP.
XX	
AC	AAAF24583;
DT	20-APR-2001 (first entry)
DE	Nucleotide sequence of the wheat Mlo protein Trm1o1.
XX	
KW	Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW	powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX	
OS	Triticum sp.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	176..1780
FT	/tag= a
FT	/product= "Mlo protein"
XX	
PN	WO200078799-A2.
PD	
PD	28-DEC-2000.
XX	
Pf	16-JUN-2000; 2000WO-EP05576.
XX	
PR	18-JUN-1999; 99US-0336112.
XX	
PA	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX	
PI	Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI	Vernooij BT, Levin JZ, Helfetz PB, Patton DA, Que Q;
XX	
DR	WPI; 2001-112311/12.
DR	P-PSDB; AAB31250.
XX	
PT	Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT	producing fungal resistant plants, in particular wheat plant -

XX Claim 2; Page 88-90; 128bp; English.
PS
XX
CC The present sequence encodes a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant phenotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.
XX
SQ Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other;

Query Match	82.2%;	Score 1316.8;	DB 22;	Length 1868;
Best Local Similarity	90.3%;	Pred. No. 4.8e-271;		
Matches 1431; Conservative	0;	Mismatches 147;	Indels 6;	Gaps 22;

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+ ||||| ||||| |||| | |||| | ||||| ||||| +
Db 260 atcatcgtgtccgtcctctcttgagacacgcgcgttcataaagctcgycattgttccacaag 319

QY 142 cggcacaaagaagcgccctgtgaggcgcctggagaagatgaagcgagactcatgctgtg 201
||||||| || ||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 320 cggcacaaagaacgcgctgycggagcgctgaggagaagatcaagcgagactcatgctgtg 379

QY	202	ggcttcataatccctgctgcctcatcgtgcacgacgaccccatcatcgcgccaagatatgcatc	261
Db	380	ggcttcatactgcgtctgctgcgcgctgacgcagacccc--catctcgggatatgcatc	436

QY 262 tccgagatgccgcgcagctatgtgcccctgcagcgcgcgcagcagggccgcagccc 3211

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Dh QY 617
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||||| |||| |

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OY 499 acctccttgaataccagtttcgcaaatgatcatctgcacggttcgcyttcacgcaccagacy 558
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QY 679 ttcatcaacgcgcattgtgcgaacaacagcaagtctgcacttccacaagtacatcaagag 738

Db	739	916
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QY	739		798
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RESULT 5
ID AAA52715 standard; cDNA; 1711 BP.
AC AAA52715;
XX 27-OCT-2000 (first entry)
DT
XX Wheat Mlo homologue putative coding sequence #4.
DE
XX Wheat; Mlo homologue; disease resistance; ss.
KW
XX Triticum aestivum.
OS
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FH Key Location/Qualifiers
FT CDS 1..1605

FT /*tag= a
ET /product= "Mlo homologue"
XX
PN WO200036110-A2.
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PD 22-JUN-2000.
XX
XX 17-DEC-1999; 99WO-US30181.
PF
PR 18-DEC-1998; 98US-0112737.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
DR WPI; 2000-431590/37.
DR P-PSDB; AAB01805.
XX
PT New polynucleotide encoding a Mlo homologue polypeptide, useful for
creating transgenic plants with altered levels of disease resistance -
PS Claim 2; Page 64; 79pp; English.
XX
CC The present sequence is a putative coding sequence for a Mlo homologue
from wheat. It was identified by searching a root and leaf cDNA library
for sequences encoding proteins similar to Mlo from Hordeum vulgare
(barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC priming of disease resistance even if the pathogen is not present. The
CC gene and protein can be used to create transgenic plants which have
increased disease resistance, as well as allowing researchers to find
other resistance-conferring genes and proteins.
CC
SQ Sequence 1711 BP; 377 A; 505 C; 473 G; 356 T; 0 other;

Query Match 82.1%; Score 1315.2; DB 21; Length 1711;
Best Local Similarity 89.8%; Pred. No. 1e-270;
Matches 1436; Conservative 0; Mismatches 158; Indels 6; Gaps 2;
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Db 9 ggactacgagtaacccccgcgcggagcgtgcgcgagacgcgctcgtggcggtgcgct 68
|||||
QY 66 ggtcttcgcgcgcacatggtgtcgtgtcgtcctcatgtgaacacggcctccacaagctcgg 125
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QY 963 ggtcagagcccaagcaaatctctctgttccaccgccccgactgggtcctcttctcat 1022
Db 966 ggttgagcccaagcaaatctctctgttccaccgccccgactgggtcctcttctcat 1025
QY 1023 acaacctgacgtgttccagaacgcgttccagatggcgcaatttgtgtgagacagtgccac 1082
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QY 1263 caactggcggaaacacgcgccaaggagaagaagaagtccgagacacgcagacatgtgtgtgc 1322
Db 1266 caactggcggaaacacgcgccaaggagaagaagaagtccgagacacgcagacatgtgtgtgc 1325
QY 1323 tcagatgatcgcgagcgcaaacaccgagcgaggtcgtcgcgcgcatgcccggggtctc 1382
Db 1326 gcagatgatcgcgagcgcgacgcccagcgagcgacgctgcgcgcatgcccggggtctc 1385
QY 1383 atcaaccgtgcacctgtcttaacaaggcgatggggcggtcggagcagccccagagcgcgcc 1442
Db 1386 gtcaaccgtgtcacctgtcttaacaaggcgatggggcggtcggagcagatccccagagcgcgcc 1445
QY 1443 caacttcgccaaggaacccaggaaggaggtcaggaacatgttaaccgggttgtgtggcgcaacc 1502
Db 1446 gacctgcgccaaggaacccatggaaggaggtcaggaacatgttaaccgggttgtgtggcgcatcc 1505
QY 1503 ggtgcacagactaaatcctaacgacaggaaggaggtccgctcgtcgtcggccctcgaaagc 1562
Db 1506 cgtgcacagactaaatcctcgtcagcagggcggaaggtcgtcctcgtcgcgcatcgtatgc 1565
QY 1563 cgacatccccaggtcgagattttctccttcagccaggggatga 1602
|||||

Db 1566 cgacatccccagcgagattttctccttcagccagggatga 1605
RESULT 6
AAZ30410
ID AAZ30410 standard; DNA; 1692 BP.
XX
XX AAZ30410;
XX AC
XX 21-DEC-1999 (first entry)
DT
XX
DE Wheat Mlo fungal resistance gene TrMlo2.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW Mlo; Erysiphe graminis; powdery mildew; ss.
XX
OS Triticum sp.
XX
FH Key Location/Qualifiers
FT CDS 1.1605
FT /*tag= a
FT /product= "fungal resistance protein Mlo2"
FT /transl_except= (pos:502..504, aa;Xaa)
FT /note= "Xaa = unknown"
XX
PN WO94.7552-A2.
XX PD 23-SEP-1999.
XX PF 17-MAR-1999; 99WO-EP01779.
XX PR 17-MAR-1998; 98US-0042763.
XX PA (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI: 1999-571820/48.
DR P-PSDB; AAY26967.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
PT
XX
PS Claim 2; Page 63-65; 102pp; English.
XX
CC This sequence represents the coding region for the wheat fungal
CC resistance gene TrMlo2. The Mlo protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new Mlo sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX
SQ Sequence 1692 BP; 360 A; 505 C; 471 G; 355 T; -1 other;

Query Match 82.1%; Score 1314.8; DB 20; Length 1692;
Best Local Similarity 89.7%; Pred. No. 1.3e-270;
Matches 1435; Conservative 1; Mismatches 158; Indels 6; Gaps 2;

QY 6 ggaacaaaaagggtgcgcggcgcgagctgcgcggagacgcgcgtcgtggcggtggcgt 65
Db 9 ggactacgagtaacccccgcgcggcgagcgtgcgcggagacgcgcgtcgtggcggtggcgt 68
QY 66 ggtcttcgcgcgcagatgtgtcgtgtcgtcctcatgtgaacacgagcctccacaagctcgg 125
Db 69 cgtcttcgcgcgtcatgatcatcgtgtcgtcctcctgtgagcagcgctccacaagctcgg 128
QY 126 ccattgttccagcaccgacaaagaagcgccctgtgggaaggcgctggagaagatgaagcg 185

Db	129	ccatttggttccacaagcgcgcacaaagaaocgctgcgcgagcgctggagaagatccaagc	188
QY	186	ggagctcatgtgtgtggtctcatatccctgtctctcatcgttcacgcagagcccatcat	245
Db	189	ggagctgatgtgtgtgggttcattctgtctgtctgcgcgtgacgcaggaacc--aat	245
QY	246	cgcacaagatatgtatctccgaggatgcccgcgaactgcatgtgcccctgcagcgcgcaac	305
Db	246	ctccgagatatgtcatctccgagaagccgcgcagcatcatgcgccctgcagcctgcccc	305
QY	306	cgaaggccgcgaagcccaagtaagtaagttgactactgccc--ggaggccaaggtgcgct	362
Db	306	tgtgtccgtcaagagcaagtaacaagaactactactgcgccaaaaaaggcgcaaggtgct	365
QY	363	catgtccaacggcgagcttgcaaccagctgcacgtctctcatctctgtgtcgcgcgtctcca	422
Db	366	aatgtccaacggcgagcttgcaaccagctccaagatgtlcatctctgtgtcgcgcgtctcca	425
QY	423	tggtcacctacagcgttcataccaatagctctctaaagccgtctcctcaaatatgaaacatgaa	482
Db	426	tggtcacctacagcgttcataccaatagctctctaaagccgtctcctcaaatatgaaacatgaa	485
QY	483	atgggagacagagaaacacccctccttggaaataaccagttcgcaaatgatcctgcagcgttcg	542
Db	486	atgggagacagagaaacccgctcctcttggaaataaccagttcgcaaatgatcctgcgcgttcg	545
QY	543	gttcaacgcacagaacgctcggttcgtgaagcgccacctggygcctctccagcaccctgacat	602
Db	546	cttcaacgcacagaacgctcggttcgtgaagcgctcaacctggygcctctccagcaccctgacat	605
QY	603	eagatgggtgtgtgcctctcttcaggcagttcttcaggttcagttcacccaaggtgtaacct	662
Db	606	cagatgggtgtgtgcctctcttcaggcagttcttcaggttcagttcacccaaggtgtaacct	665
QY	663	gaccttgaggcgagcgttcatacaacgcgcatttgtcgcaaaacagcaagttcgacttcca	722
Db	666	caccttgaggcgagcgttcatacaacgcgcatttgtcgcatatacagcaagttcgacttcca	725
QY	723	caagttacatcaagaggtcgtatggagagcgaacttcaaggtcgtcgtcgcatcagccctccc	782
Db	726	caagttacatcaagaggttccatgtgagagcgaacttcaaaagtcgtcgttgcatcagccctccc	785
QY	783	gctgtggggtgtgcgatcctctcaaccctctctcttgacatcaatggggttggcagcgtcat	842
Db	786	gctgtgtgtgtgcgatcctctcaaccctctctcttgatataatgacggatcggcagcgtctcac	845
QY	843	ctggaattcttcatccctctcgtgatccctctctgtgtgttggaaaccaagctggagatgat	902
Db	846	ctggaattcttcatccctctcgtgatccctctctgtgtgttggaaaccaagctggagatgat	905
QY	903	catcatggagatgcccctggagatcccaaggacccggcgagcgtcatcaagggggccccgct	962
Db	906	catcatggagatgcccctggagatcccaaggacccggcgagcgtcatcaagggggccccgct	965
QY	963	ggtcgaagcccaagcaacaagtctctctgtgttccaccgccccgagctggtctcttctcat	1022
Db	966	ggttgagcccaagcaacaagtctctctgtgttccaccgccccgagctggtctcttctcat	1025
QY	1023	acaacctgacgttgttccagaacgcgttccagatggcgacatttgtgtgacagatggccac	1082
Db	1026	acaacctgacgctgttccagaatgcgttccagatggcacatttcgtctgacagatggccac	1085
QY	1083	gcccgcgttgaagaatatgtactacaacgcagatcgggcgtgagcatcatgaaggtgtgtgt	1142
Db	1086	gcccgcgttgaagaatatgtcttccatatgacacatcggtctgagcatcatgaaggtgtgtgt	1145
QY	1143	ggggtatgctctccagttcctctgtcagctatatatgaccttccccctctacgcgctcgctcac	1202
Db	1146	ggggtatgctcttccagttcctctgtcagctatatatcaccttccccctctacgcgctcgctcac	1205
QY	1203	acagatgggatccaacaatgaagaaggtccatcttgcagcagcagacgcttccaaggcgctcac	1262

Db	1206	acagatggtatcgaacatgaaaggttcattcttcgacgagcagacggtccaaagcgctgac	1265
QY	1263	caactggcggaacacggtccaagagaaagaaagatcccgagacacgagacatgtctgatgac	1322
Db	1266	caactggcggaacacacggtccaagagaaagaaagatcccgagacacgagacatgtctgatgac	1325
QY	1323	tcaagatgatcgcgcgacgcacaacacccgagccgaggtctcgccgatatgcgcgaggtcgctc	1382
Db	1326	gcagatgatcgcgcgacgcgcagccgagccgagccgagccagtcgcgatatgctagcccggtctc	1385
QY	1383	atcacccgtgcacctgtcttcacaaaggagcatggtggcgtctcgagcagacccccagagcgcc	1442
Db	1386	gtcacccgtgtcacctgtcttcacaaaggagcatggtgaaggtctcgagcagatccccagagcgcc	1445
QY	1443	caactcgcgaaggaacccagagagaggttaggagacatgtacccggtgtgtgtgcgaccc	1502
Db	1446	gacctcgcgaaggaaccatgtgagagaggttaggagacatgtacccggtgtgtgtgcgaccc	1505
QY	1503	gtgtgcacagactaaatctctaacgacagagaggtccggtctgtctgcgacctcgaaac	1562
Db	1506	cggtgcacagactaaatctctgtgacagcgcgaggtcggtctctctgtcgcacatcgatgc	1565
QY	1563	cgacatcccccagtgccagattttctcttcagccagggatga	1602
Db	1566	cgacatcccccagcgccagattttctcttcagccagggatga	1605

RESULT	7
AAAF24584	
ID	AAF24584 standard; DNA; 1693 BP.
XX	
AC	AAF24584;
DT	20-APR-2001 (first entry)
XX	
DE	Nucleotide sequence of the wheat Mlo protein TrMlo2.
XX	
KW	Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae; powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX	
OS	Triticum sp.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1605
FT	/tag= a
FT	/product= "Mlo protein"
FT	/transl_except= "(pos: 502..504, aa: Xaa)"
FT	/note= "Xaa is an unspecified amino acid"
XX	
PN	WO200078799-A2.
XX	
PD	28-DEC-2000.
XX	
PF	16-JUN-2000; 2000WO-EP05576.
XX	
PR	18-JUN-1999; 99US-0336112.
XX	
PA	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX	
PI	Salmeron JM, Weisio LJ, Strawn LJ, Kramer CM, Wang HX; Vernoolf BT, Levin JZ, Heifetz PB, Patton DA, Que Q;
XX	
DR	WPI; 2001-112311/12.
DR	P-PSDB; AAB31251.
XX	
PT	Novel polynucleotide which encodes Mlo protein from wheat, useful for producing fungal resistant plants, in particular wheat plant -
XX	
PS	Claim 2; Page 92-94; 128pp; English.
XX	
CC	The present sequence encodes a Mlo protein. Mlo proteins given resistance to fungal pathogens which infect living epidermal plant cells.

Mlo proteins give proteins resistance to fungal pathogens, especially Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo locus are responsible for a plant resistant pathotype. The mechanism of Mlo resistance involves the formation of large cell wall appositions called papillae, at pathogen contact sites. Papillae mainly contain callose, but also carbohydrates, phenols and proteins. Polynucleotides encoding Mlo proteins are useful for making transgenic plants, preferably wheat, which are resistant to fungal pathogens.

SQ Sequence 1693 BP; 360 A; 505 C; 472 G; 355 T; 1 other;

Query Match	82.1%;	Score 1314.8;	DB 22;	length 1693;
Best Local Similarity	89.7%;	Pred. No. 1.3e-270;		
Matches 1435; Conservative	1;	Mismatches 158;	Indels 6;	Gaps 2;

OY 6 ggacaaaagggtgcgagcgagcgtctcttgccgttggcagt 65
 |||| | ||||||| ||||||||||| |||||||||||
Db 9 ggaactacgatccccccgcgcgcgcgcgtctcttcgtggccgttgccgt 68

QY 66 ggtcttcgcgcgcacatggtgtcgttcgtctcatatgaaacacgacctccacaagctcgg 125
||||||| ||| | ||||||||| ||| ||| |||||||||
Db 69 cgtcttcgcgcgcacatgatcatcgtgtcgtctctcctgtgaagacgcgcctccacaagctcgg 128

QY 126 ccatttggtccacgcaaccgcgaacaagaagcccttctggagcgcctgtgagaatgatgaagc 185
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 ccattggttcacaacgcgcgaacaagaagcctgtcgcgagcgcctgtgagaatcatcaagc 188

DY 186 ggagctcatgctgttggtcctacataccctgcctcctaactgaaggaccatcaat 245
 ||||| |
Db 189 gtagctgatcggtgggttcattcacctcgtctgctgcgccgtaaacgcagaacct--aat 245
 ||||| |

QY 246 cgcgaagatattgatctccgaggatgcccgacgtcatgtggccttgcagaagcgcgcac 305
 | | | | | | | | | | | | | | | | | | | | | |
Db 246 ctccggatatgcatctccgagaagcgcccaagcatcatgtcgccctgcagacctgcccc 305

OY 306 cgaagggccgcgaagcccagaagtagcttgactactgccc--ggaaggcgaagtgtgcgct 362
 | | ||| | | | | | | | | |
Dd 306 tggtttcgtcaagagcgacgtaccacaagactactactgcygccaaaaagggcgaagtgtgcgt 365

QY 363 cagtccacgggcagcttgcaaccagctgcaagcttcattctcgtgctgcggtctcca 422
 |||||
 Db 366 aatgtccacgggcagcttgcaaccagcttcacatgtttcattctcgtgctgcgcggtctcca 425
 |||||

QY	423	tg	tca	ccta	cag	cg	tca	tca	ccata	gct	cta	ag	ccg	ctc	caaa	atg	aa	cat	g	aa	ga	aa	482
Dd	426	tg	tca	cccta	cag	cg	tca	tca	ccata	gct	cta	ag	ccg	ctc	caaa	atg	aa	cat	g	aa	ga	aa	485

OY 483 atggagacagagaccacctctctgtgataccagttgcgaatgatcctgcacgyrttcg 542
 ||||| : |||||
Db 486 atggagacagagaccgytctcttgataccagtctgcgaatgatcctgcgcggttcg 545

OY		543	gttcacgaccagacgtctcgtgaagcgccacctgggcctctccagcaccccgcgat	602
Dd		546	ccticacgcaccagacgtctcgtgaagcgtlcaacttgycctcttccagcacccccggcat	605

QY 603 cagatggtgtgtgcctcttcaggcagttcttcagtcagtcaccaaggtgatacct 662
 |||||
 Db 606 cagatggtgtgtgcctcttcaggcagttcttcagtcagtcaccaaggtgatacct 665

Dy 663 gacctgaaggcgagctcatcaacgcgcatltytcgcaaaacagcaagtgcattcca 722
||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db 666 caccctgaggcgagcttcatcaacgcgcatltytcgcaataacagcaagtgcattcca 725

QY 723 caagtaacatcaagaggtcgatggaaggaacgactcaagtcgtcgatcgatcagctccc 782
|||||
Db 726 caagtaacatcaagaggtcgatggaaggaacgactcaagtcgtcgatcgatcagctccc 785
|||||

QY	783	gctgctggggtgtgtgcgataccccaacccctctccttgatacaatggtggtgcacgctcat	842
Db	786	gctgtgtgtgtgtgcgataccccaacccctctccttgataatgacggtatcgcaacgctcac	845

QY 843 ctgattcttcatccctccgtgatccctctgtgtgttgaaccaagctgagatgat 902

Db 846 ctgagattcttcatccctctcgtaacctcttqqtqatgaacaaqctgaaatga

QY	903	catcatgtgagatg	gccctgtgagatc	ccagaccggcgagc	gtcatcaaggggccc	cgt	962
Db	906	catcatgtgagatg	gccctgtgagatc	ccagaccggcgagc	gtcatcaaggggccc	cgt	965

QY	963	ggtcgcagccacagaatctctctgttccaccgcgccgcactggtccctctctcat	1022
Db	966	ggttcgcagccacagaatctctctgttccaccgcgccgcactggtccctctctcat	1025

QY 1023 acacctgacgttgttcagaagcgtttcacatgycatttgttgacagtggccac 1082
||||||| ||||||| ||||||| ||||||| |||||||
Db 1026 acacctgacgctgttccagaatcgcttcagatgycacattcgctctgacacatggccac 1085

OY 1083 gccgcgcttgaagaatgtaccacacgcagatcggcgctgagcatcatgaagtgtgtg 1142
|||||
|||
Db 1086 gccgcgcttgaagaatgtccatcatgatgcacatcggtcttaagcatcatgaagtcgtgt 1145

QY	1143	ggggctagctctccagttcctctgcagtatatgaccttcccccttaagcgctcgtcac	12022
Db	1146	ggggctgctcttcagttccctctgcagtatatcaaccttccccctctaagcgctcgtcac	12055

OY 1203 acagatggtgaacaacatgaagggttcattctgcagcgacagcgtccaagcgctaac 12622

Db 1206 acagatgggatcgaaacatgaagggttcattctgcagcgacagcgccaaagcgctaac 12655

QY	1263	caactggcggaacacacgcgaaggagaagaagatcgcgagacacgcgacatgctgtatggc	1322
Db	1266	caactggcgggaacacacgcgcgaaggagaagaagatccgagacacgcgacatgctgtatggc	1325

[illegible]

OY	1383	atcacccgtgacactgcttcacaagggcatgtggcgctcgcagaccocccagagcgccc	1442
Db	1386	gtcacccgtgcacctgtcttcaacaaggcatgtggacgcttcgcagcatccccagagcgccc	1445

[illegible][illegible]

OY 1563 cgacatcccccagtgccagattttccttcacgccaagtga 1602
|||||
Db 1566 cgacatccccacgcgcagatttttccctcacgccagaatatga 1605

RESULT	8
AAZ30411	
ID	AAZ30411 standard; DNA; 1886 BP.

AC	AAE30411;
XX	
DT	21-DEC-1999 (first entry)

DE wheat M10 fungal resistance gene Trm103.
XX
XW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;

Host	Pathogen	Location	Year	Reference
KW	Mlo; Erysiphe graminis; powdery mildew; ss.	France	1950	1
XX				
OS	Triticum sp.			

Accession	Protein	Accession	Protein
130..1802	/+tag= a	130..1802	/+tag= a
FT	/product= "fungal fusion protein M103"	FT	/product= "fungal fusion protein M103"
XX		XX	

PN WO9947552-A2.
XX 23-SEP-1999.
PD
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI; 1999-571820/48.
DR P-PSDB; AAY26968.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 68-70; 102pp; English.
XX
CC This sequence represents the coding region for the wheat fungal
CC resistance gene TrMlo3. The Mlo protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new Mlo sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX
SQ Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Query Match 81.5%; Score 1305.6; DB 20; Length 1886;
Best Local Similarity 89.9%; Pred. No. 1.2e-268;
Matches 1424; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

QY 22 ccggcgcggagctgcgcggaagccgtctgtggcggtggtgtcttcgcgcgcatg 81
Db 222 ccgcgcggagcgtgcgcggaagccgtctgtggcggtggtgtcttcgcgcgcatg 281
QY 82 gtgtctgtgtccgtccatcgtgaacagcgctccacaagctcgccattgttccagcac 141
Db 282 atcatcgtctccgtccctcctcgtgagcagcgctccacaagctcgccattgttccacaag 341
QY 142 cggcacaagaagccctgtgaggcgctggagaagatgaagcgagctcatgtgtgtg 201
Db 342 cggcacaagaagcgctgagcgagcgctggagaagatgaagcgagctgtgtgtg 401
QY 202 ggtctcatatccctgtctcctcatcgttcaagcagaccatcatcgtccaagatatgcac 261
Db 402 ggaattcatctcgtctgtctgcgcgttcaagcaggaacc--aatctccgggatatgcac 458
QY 262 tcgagagatgcgcgcgacgtcatgtgcccctgcaagcgcgcaagcgaggccgcaagccc 321
Db 459 tcccaagaagcgccgacgatcatgtgcgcctctgcaaggtggaaccgcgttccgtlcaagagc 518
QY 322 agcaagtactgtactatgccc--ggaaggcaaggtgagcgctcatgttccaagggcagc 378
Db 519 aagtacaaggaactactatgcgcacaaggggcaaggtgagcgctcatgttccaagggcagc 578
QY 379 ttgcaccagctgcaagcttcatcttcgtgtcgcggtcttcctcatgttcaacctacagcgtc 438
Db 579 ctgcaccagctccaacatatattcatcttcgtgttagcgcttcttcattcaacctacagcgtc 638
QY 439 atcacaatagctctaagcgctctcaaaatgagaacatggaagaatgagagacagagacc 498
Db 639 atcatcatgtctctaagcgctctcaagatgagaacatggaagaatgagagacagaaacc 698
QY 499 acctccttgaataaccagttcgaatatgatcctgtcacggttccggttccagcacccagagc 558
Db 699 gcctccttgaataaccagttcgaatatgatcctgtcgcggttccggttccagcacccagagc 758

QY 559 tcgttcgtgaagcgccacactgggcctctccagcaccccttggcatcagatgggtgtggcc 618
Db 759 tcgttcgtgaagcgccacactgggccttccagcaccccttggcatcagatgggtgtggcc 818
QY 619 ttcttcagcgacttcttcaggtcagtcacccaaggttgactactgaccttgaaggcaggc 678
Db 819 ttcttcagcgacttcttcaggtcagtcacccaaggttgactactgaccttgaaggcaggc 878
QY 679 ttcatcaacgcgcatltgtgcgcaaaacagcaagttcgacttccacaagtlacatacaagag 738
Db 879 ttcatcaacgcgcatltgtgcgcaaaacagcaagttcgacttccacaagtlacatacaagag 938
QY 739 tcgattgaggaagcacttcaaggtcgtcgtgcgcatcagcctcccgctgtgtgggtgtggcg 798
Db 939 tccattgaggaagcacttcaaaagtcgtcgttgcatcagcctcccgctgtgtgggtgtggcg 998
QY 799 atcctcaccccttctccttgacatcaaatggggttgcaagctcatctggattcttccatc 858
Db 999 atcctcaccccttctccttgatatacgaggtatcggaacatacctggttcttccatc 1058
QY 859 ccttcgtgatacctctgtgtgttggaaccaagcttgagatgatacatcatgagatggcc 918
Db 1059 ccttcatacatcctctgtgtgttggaaccaagctagagatgatacatcatgagatggcc 1118
QY 919 ctggagatocaggaacggcgagcgctcatcaagggggcccccggtgtcgaagccagcaac 978
Db 1119 ctggagatocaggaacggcgctcatcaagggggcccccggtgtcgaagccagcaac 1178
QY 979 aagttcttctgttccacccgcccagactgggtctctcttctcatcacactgacgtgttc 1038
Db 1179 aagttcttctgttccacccgcccagactgggtctctcttctcatcacactgacgctgttc 1238
QY 1039 cagaacgcgttccagatggcgcatlttgtgtgacaggtggccaagccccggttgaagaa 1098
Db 1239 cagaacgcgttccagatggcgcatlttgtgtgacaggtggccaagccccggttgaagaa 1298
QY 1099 tgtctacaacagcagatcgggctgaagcatcatgaaggtgtgtgtgggtagcttccag 1158
Db 1299 tgtctacaatgaacatcgggctgaagcatcatgaaggtgtgtgtgggtagcttccag 1358
QY 1159 ttctctgcagctatatgaccttccccctctacgcgctcgttccacacagatgggatcaaac 1218
Db 1359 ttctctgcagctatatgaccttccccctctacgcgctcgttccacacagatgggatcaaac 1418
QY 1219 atgaagaagttccattcttcgacgagcagacgcttccaaggcgctccaactggcggaacag 1278
Db 1419 atgaagaagttccattcttcgacgagcagacgcttccaaggcgctccaactggcggaacag 1478
QY 1279 gccaaaggaaagaagaagttccgaagacaagacatgtgtatgtctcagatgcggcgac 1338
Db 1479 gccaaaggaaagaagaagttccgaagacaagacatgtgtatgtctcagatgcggcgac 1538
QY 1339 gcaacaccgagccgagcgctcgtcccgatgcccagcggggttccatcacccggtgcacctg 1398
Db 1539 gcaacaccgagccgagcgctcgtcccgatgcccagcggggttccatcacccggtgcacctg 1598
QY 1399 ctccacaagggcattggggcggttcgagcagacccccagagcgcgccacactgcgaagagcc 1458
Db 1599 ctccacaagggcattggggcggttcgagcagacccccagagcgcgccacactgcgaagagcc 1658
QY 1459 cagcaggaaggttaggagacatgtaccgggttgtgtgagcgaaccgggtgcacagactaat 1518
Db 1659 atgaggaaggttaggagacatgtaccgggttgtgtgagcgaaccgggtgcacagactaat 1718
QY 1519 cctaacgacaggaaggaggtccgcctcgtcgtcgcgcctcgaagccgacatcccagtgca 1578
Db 1719 cctgtgacagggcgaggtcgtctcttcattcagccctcgtatgcgacatcccagtgca 1778
QY 1579 gatttttcttcagccagggatga 1602
Db 1779 gatttttcttcagccagggatga 1802

RESULT 9
AAF24585
ID AAF24585 standard; DNA; 1886 BP.
XX AAF24585;
XX AC
XX 20-APR-2001 (first entry)
XX
XX Nucleotide sequence of the wheat Mlo protein TrmMlo3.
XX
XX
XX Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
XX powder mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX
XX Triticum sp.
XX
FH Key Location/Qualifiers
FT CDS 198..1802
FT /*tag= a
FT /product= "Mlo protein"
XX
XX WO200078799-A2.
XX
XX PD 28-DEC-2000.
XX
XX PF 16-JUN-2000; 2000WO-EP05576.
XX
XX PR 18-JUN-1999; 99US-0336112.
XX
XX PA (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
XX PI Vernooij BT, Levin JZ, Helfetz PB, Patton DA, Que Q;
XX
XX DR WPI; 2001-112311/12.
XX P-PSDB; AAB31252.
XX
XX PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
XX producing fungal resistant plants, in particular wheat plant
XX
XX PS Claim 2; Page 97-99; 128pp; English.
XX
XX CC The present sequence encodes a Mlo protein. Mlo proteins given
XX CC resistance to fungal pathogens which infect living epidermal plant cells.
XX CC Mlo proteins give proteins resistance to fungal pathogens, especially
XX CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
XX CC locus are responsible for a plant resistant phenotype. The mechanism
XX CC of Mlo resistance involves the formation of large cell wall appositions,
XX CC called papillae, at pathogen contact sites. Papillae mainly contain
XX CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
XX CC encoding Mlo proteins are useful for making transgenic plants,
XX CC preferably wheat, which are resistant to fungal pathogens.
XX
XX SO Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Query Match 81.5%; Score 1305.6; DB 22; Length 1886;
Best Local Similarity 89.9%; Pred. No. 1.2e-268;
Matches 1424; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

QY 22 ccggcgcgaggagctgcgcggagagccgcgtctgtggcggtgtgcgtgtcttcgcgcgcac 81
Db 222 ccggcgcgagagctgcgcggagagccgcgtctgtggcggtgtgcgtgtcttcgcgcgcac 281
QY 82 gtgtctgtgtcgtcttcacatggaacagcgctccacaagctcggccattgtttccagcac 141
Db 282 atcatcgtctcgtctctctctgtgagcaagcgctccacaagctcggccattgtttccacaag 341
QY 142 cggcacaagaagccctgttggagcgctgtgagaagatgaagcgagctcatgtgtgtg 201
Db 342 cggcacaagaagcgctgtgagcgcgctgtgagaagatgaagcgagcgagctgtgtgtgtg 401

QY 202 ggcttcataatccctgtctctcatcgtcagcgagaccaccatcatcgccaagatatgtatc 261
Db 402 ggatlcataatcgtctgtctcgcgcgtcagcgagacc---aatctcgggatatgtatc 458
QY 262 tccgagatgcgcgcgcgacgtcatgttggcccttgcaagcgcggaaccgagggccgcaagccc 321
Db 459 tcccagaagggccgcgcagcatcatgtgcccccttgcaaggtgaaaccccggttcgttcaagagc 518
QY 322 agcaagtaacgttgaactatgccc---ggaggcaaggttgcgctcatatgtccacggggcagc 378
Db 519 aagtaacaaggactactactgcgcacaagaagggcaaggttgcgtcatatgtccaagggcagc 578
QY 379 ttgcaccagctgcagcgtctcatcttctgtgtgtcgcggtcttccatgttcaactacagcgtc 438
Db 579 ctgcaccagctccacatatcatcttctgtgtgttagccggtcttccatgttcaactacagcgtc 638
QY 439 atcaccatagctctaagccggtctcaaaatgagacaatggaagaatgagagacagagacc 498
Db 639 atcatcatgtctctaagccggtctcaagatgagacaatggaagaatgagagacagagacc 698
QY 499 accctcttggaaataccagttcgcacaatgatctcctgcagcggttcgggttcaagcaccagacg 558
Db 699 gccctccttggaaataccagttcgcacaatgatctcctgcgcggttccggttcaagcaccagacg 758
QY 559 tcgttcgttgaagcgccacccttggcctctccagcacccttggcatcagatgtgtgtgtgcc 618
Db 759 tcgttcgttgaagcgccacccttggcctcttccagcacccttggcgttcagatgtgtgtgtgcc 818
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QY 859 cctctcgtatcctcttgtgtgttggaaaccaagcttggagatgatcatcatgagatggcc 918
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QY 919 ctggagatccaggaacggcgagcgtcatcaagggggcccccggtgtgcagcccaagcaac 978
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QY 979 aagttcttctgttccaccgcccccgacttgggtctcttcttcatcacactgaactgtgttc 1038
Db 1179 aagttcttctgttccaccgcccccgacttgggtctcttcttcatcacactgaactgtgttc 1238
QY 1039 cagaacgcgttccagatggcgcatlittgttggacagttggccaagcccggttgaagaa 1098
Db 1239 cagaacgcgttccagatggcgcatlittgttggacagttggccaagcccggttgaagaa 1298
QY 1099 tgctacacacgcagatcgggtgagcatcatgaaggtgtgtgtgtgggttagctcttcag 1158
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QY 1219 atgaagagttccatcttcgaacgcagcagacgttccaagcgcttcaccaacttggcgaacag 1278
Db 1419 atgaagagttccatcttcgaacgcagcagacgttccaagcgcttcaccaacttggcgaacag 1478
QY 1279 gccaaaggagaagaagaagtcgcgagacacggaacatgtgtgtgtcatgatcgtcgcgac 1338

|||||
Db 1479 gccaaaggagaagaaggtcccgagacacgacatgctgtagcgacatgacgcgcac 1538
QY 1339 gcaacaccgagcgaggtcgtcgcgcgacgtccgagccggggtcatcacccgtgcacctg 1398
Db 1539 gcaacaccgagcgaggtcgtcgcgcgacgtcccgatgctagccggggtcatcgccggtgcacctg 1598
QY 1399 ctccacaaggagcagtggtcgtcgcgcgcacccccagagcgcgcccaactcgccaagacc 1458
Db 1599 ctccagaaggagcagtggtcgtcgcgcgcacccccagagcgcacccactcgccaagacc 1658
QY 1459 cagcagagagctagggacatgtacccggtgtgtggtgcgcacccggtgcacagactaat 1518
Db 1659 atggagagagctagggacatgtacccggtgtgtggtgcgcacccgtgtacacagactaat 1718
QY 1519 cctaacgacagagaggtccgcctcgtcgtcgcgcctcgaaagccgacatccccagtga 1578
Db 1719 cctgctgacagcgaggtcgtcctctcatcacagccctcgatgcgcacatccccagcgca 1778
QY 1579 gattttccttcagccaggatga 1602
Db 1779 gattttccttcagccaggatga 1802
RESULT 10
AAV35030
ID AAV35030 standard; cDNA; 1635 BP.
AC AAV35030;
XX 13-OCT-1998 (first entry)
DE Hordeum vulgare MLO gene homologue.
XX Hordeum vulgare.
KW Barley; MLO; mildew; pathogen; resistance; ss.
OS Hordeum vulgare.
FH Key Location/Qualifiers
FT CDS 1..1635
FT /tag= a
FT /product= MLO protein homologue
XX WO9804586-A2.
XX 05-FEB-1998.
XX 29-JUL-1997; 97WO-GB02046.
XX 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX Bueschges R, Panstruga R, Schulzelefer PMJ;
XX WPI; 1998-159149/14.
DR P-PSDB; AAW59445.
XX New isolated MLO gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
PT Claim 9; Fig 11; 150bp; English.
XX The sequence is that of a homologue of the MLO gene, wild-type MLO
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of MLO function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to

CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 1635 BP; 315 A; 496 C; 520 G; 304 T; 0 other;
Query Match 58.5%; Score 936.8; DB 19; Length 1635;
Best Local Similarity 76.4%; Pred. No. 3.8e-190;
Matches 1270; Conservative 0; Mismatches 272; Indels 120; Gaps 5;
QY 18 ggtgccgagcgaggagctgcggagagcgctcgtggcggtggtgcttcgcgcgc 77
Db 12 ggcggagagtcgggagctgtcgacacgcccgaactggtggcggtggtgctgctgcgcgc 71
QY 78 catgtgtcgtgtccgtccatcagacacgagccctcacaaagctcggccattgttcca 137
Db 72 catgatactgtctcgtcgcgcacgtgagacgagcgctccacaagctcggccaactgttcca 131
QY 138 gcaccgacacaagaagccctgttgggagcgctggagaagatgaagcgagctcatgtct 197
Db 132 caagtggcgacaagaagggcccttggggagcgctggagaagatgaagcgagctcatgtct 191
QY 198 ggtggcttcataatccctgtcctcctcgtcagcagagaccccatcatcgccaagatatg 257
Db 192 ggtggcttcataatccctgtcctcctcgtcagcagagatcc---cgttcacagatctg 248
QY 258 catctccgagagatgcgcgcgagcgtcatgtggccctgcaagc-----gcggcacgagag 311
Db 249 catctccaaaggagcgcgagagaagatgtccctgtgaagccttaagcagcgcgccgag 308
QY 312 ccgcaagcccagaagta----- 329
Db 309 tggcaaaaggagaagacatcacccggagcttctcgtcgtccaaagcgagagcgagaccca 368
QY 330 -----cgtgactactgcgcggaggcgcaagtgtgc 359
Db 369 ccgccggttcctgtgtgcgcccgccggagtggaagctctgcgcgaacagggcaagtgtgc 428
QY 360 gctcatgtccacgggagcagcttgcaaccagctgcacgcttcatcttcgtctgcgcgtctt 419
Db 429 gctgatgtcagcgggagcatgtgcaaccaactgcaacatatcatcttcgtctgcgcgtctt 488
QY 420 ccattgtcacctacagcgtcatcaaccatagctctaagccggtctcaaaaatgagaacatgaa 479
Db 489 ccacgtcttgtacagcgtctgacacacatgaacctaacgcttccaaaatgagaacatgaa 548
QY 480 gaaatggagacagagaccacactccttggaaatcacagttcgcaaatgatcctgcacggt 539
Db 549 caagtgggagtcgagaccgcctcgtcggagatatcagttcgcaaatgatcctgcacggt 608
QY 540 ccggttcacgacccagacgctgttcgtgaagcgcaacctgggctctccagcaccctgtg 599
Db 609 ccggttcacgacccagacgacgctgttggaggcgacactgggctctccagcaccctgtg 668
QY 600 catcagatggtgtgtgacctcttcaggagagttcttcaggtcagttcacccaaggttgacta 659
Db 669 cgtcagatggtgtgtgacctcttcaggagagttcttcaggtcagttcacccaaggttgacta 728
QY 660 cctgacctgaaggcgagcttcataacgcgcaattgtgcgcaaacagcaagttcgactt 719
Db 729 cctgacctgcggcagggcttcataacgcgcaattctctgcgagggcaacaggttcgactt 788
QY 720 ccacaagtacatacaagaggtcgtgaggaagcacttcaaggtcgtcgtgcacagcct 779
Db 789 cgacaagtacatacaagaggtcgtgaggaagcacttcaaggtcgtcgtccgcacatcagctc 848
QY 780 cccgctgtggggtgtgtgcgcatcctcacccctctccttgacatcaatgggttgacagct 839
Db 849 caagctcgtgtcgtgtggcggttcctcatcctctccttgatcttcgaacgggagtcgcactct 908
QY 840 catctgatttcttcacccctcctcgtgatcctctgtgtgttggaaaccaagctggagat 899
Db 909 tctctgatatgtccgtgtgtctcctcgtgatcctctgtgtgttggaaaccaagctggagat 968

QY	900	g	a	t	c	a	t	c	a	t	g	a	t	g	c	c	c	t	g	a	a	t	c	c	a	a	g	a	c	c	c	g	c	a	g	c	t	a	c	a	a	g	g	g	c	c	c		959						
Db	969	g	g	t	a	t	c	a	t	g	a	t	g	c	c	a	a	g	a	t	c	c	a	a	g	a	t	c	a	t	a	g	c	c	g	g	a	g	a	g	c	t	g	t	c	a	a	g	g	t	c	c		1028	
QY	960	c	g	t	g	t	c	g	a	g	c	c	a	a	a	a	g	t	t	c	t	t	c	t	g	t	c	g	t	c	c	a	c	c	c	c	c	c	a	c	c	c	c	c	c	c	c	c	c	c	c		1019		
Db	1029	c	g	c	c	g	t	c	g	a	g	c	c	a	a	c	a	a	g	a	c	t	c	t	c	t	g	t	t	c	a	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c		1088			
QY	1020	c	a	t	a	c	a	c	c	t	g	a	c	g	t	g	t	t	c	c	a	a	c	g	c	g	t	t	c	a	g	a	t	t	t	g	t	g	t	g	a	c	a	t	g	c		1079							
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QY	1080	c	a	c	g	c	c	c	g	c	t	t	g	a	a	a	t	g	t	c	a	c	a	c	a	c	g	c	a	g	a	t	c	g	g	c	t	g	a	g	c	a	t	c	a	t	g	a	a	g	t	g	t		1139
Db	1149	c	a	c	g	c	c	c	g	c	t	t	g	a	a	a	t	g	t	c	a	c	a	c	g	a	a	a	t	g	c	a	a	t	g	a	t	g	a	c	a	t	g	c	c	a	a	g	t	c	g	t		1208	
QY	1140	g	g	t	g	g	g	c	t	a	g	t	c	t	c	c	a	g	t	c	c	t	c	t	c	t	g	c	a	g	t	a	t	a	t	g	a	c	t	c	c	c	c	c	c	c	c	c	c	c	c	c		1199	
Db	1209	g																																																					

RESULT	11	
AAV35028		
ID	AAV35028	standard; DNA; 1611 BP.
XX		
AC	AAV35028;	
XX		
DT	13-OCT-1998	(first entry)
XX		
DE	Oryza sativa	MLO gene homologue.
XX		
KM	Rice;	MLO; mildew; pathogen; resistance; ss.
XX		
OS	Oryza sativa.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1611
FT		/tag= a
FT		/product= MLO protein homologue
XX		
PN	MO9804586-A2.	
XX		
PD	05-FEB-1998.	
XX		

PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
XX Bueschges R, Panstruga R, Schulzelefert PMJ;
PI
XX WPI; 1998-159149/14.
DR P-PSDB; AAW59444.
DR
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
XX
PS Claim 6; Fig 10; 150pp; English.
XX
XX
CC The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen..
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 1611 BP; 348 A; 450 C; 450 G; 363 T; 0 other;

Query Match	47.8%;	Score 765.6;	DB 19;	Length 1611;
Best Local Similarity	71.5%;	Pred. No. 1.1e-153;		
Matches 1151; Conservative	0;	Mismatches 384;	Indels 75;	Gaps 8;

OY	26	cgcggagctgcccgaagaacgccgtcgttgccggtgcygtgtcttcgcgcccatggtgc	85
Db	23	cgcggagtgcggagacgcgcgacctgtggcggtgcgttcgtcgcgcgtccctgtgc	82
OY	86	tcgltgcgttctcatatgaaacacgycctccaacagctcgcattgtttccagcaaccgc	145
Db	83	tcgtctccgcgcacatgagcacgycctccacaactcagcca-----taaaccaaccgc	137
OY	146	acaagaagccccgtgtggaggcgtgtgagaagatgaagcgcgagctcatgtctgtgygct	205
Db	138	agaagttctcataatttcttgttcttatctgtcaact-----gcagagctgatgtctgtgygct	193
OY	206	tcatatccctgctcctcatctcgtcacgcagagaccccatcatcgcaccaagatatgcattccg	265
Db	194	tcatatccctgcttctcatccggtggcacagcgcc---catctcaaagatctgcattcccca	250
OY	266	aggatgcgcgcgaagtcatagtltygccttgcaag-----	297
Db	251	agtcgctgcacaacatctgtltygcgtgcaagcagcgaagatgcatcgaagaagaag	310
OY	298	-----cgcggcacccgagagcgccgaagcccaagcaagtactgtgactactgccgg	346
Db	311	cagcaagtgtgcgcggctccttgccgcgcgcgcggcgcggtgactactgtcgaaatlcg	370
OY	347	aggcgcaaggtgcgctcatgttccacgycgagcttgcaccagctgcaagcttcttcattctcg	406
Db	371	atgcaaggtgcgctgtgatgtcgcaaaagagcatgcaaccagctgcacatttccattctcg	430
OY	407	tgtcgcggtcttccatgtcacctaagcgtcatcaccatagctctaagccgttccaanaa	466
Db	431	tgctgcgctgttccatgtttaacctactgcatacattcaaccatggtttagygcgcctcaaaa	490
OY	467	tgagaacatggaagaaaaatggagacagagaccactccttgyaataaccagttcgcaaatg	526
Db	491	tgaagaatatggaagaagtlyggagtacacagaccactcattgagtatcagttcgcacatcg	550
OY	527	atcctgcacggttccggttccacgcacaccagacgtcgttcgtgaaagcgcacactgag---cc	583

||||| ||||| ||| ||||||||||| ||||||||||||||||||| || |||||
Db 551 atccttcacgattcaggttcacgcatcagacgctcgttcgtagaagcgycatctggtatcat 610
QY 584 tctccagcacccttgycatcagatgggtgtggtgccttcttcaggcagttcttcagtcag 643
Db 611 tctcaagcacccttggtcctcagatgtagtcgtatgcattcttcaggcagttcttggtcg 670
QY 644 tcaccaaggttgactaccctgaaccttgaggcgagcttcatacaacgcgcatttgtcgcaa 703
Db 671 tcaccaaggttgactaccctgaaccttgaggcgagcttcatacaacgcgcatttgtcgcaa 730
QY 704 aacgcaagttcgacttcacaagtacatcaagaggtcgatgagagcagacttcaaggtcg 763
Db 731 atagcaagttcgacttcacaataatcacatcaagaggtcttgagagcagacttcaagttg 790
QY 764 tcgtcgycatcagcctcccgctgtgtggtgtgtggtgcgaltccctcaccctcttccttgaca 823
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QY 824 atggggttgcaagcctcatctgattcttcttcacccctctcgtagatccctctgtgtgtgt 883
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Db 971 tgatccaggtgagcaccctatgtgtgaaccaagcaacagtaacttctgttcaaccgacctg 1030
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Db 1031 actggtctctgttttccatacacctgaactgttccataacgcgcatlccagatggtgcatt 1090
QY 1064 ttgtgtgacagtggtccacgcccgtgtgaagaatgtctacacacgcgagatcggtgtga 1123
Db 1091 tcgtatgactatggaacacactgtgtctgaagaatgtctccatgaataatattgtgtga 1150
QY 1124 gcatcatgaagtggt 1183
Db 1151 gcatcgtggaagtcattgt 1210
QY 1184 ccctctacgcgtcgttcacacagatggtgatcaacaatgaagaggtccatcttcgagagc 1243
Db 1211 cgctctacgcgtcgttcacacagatggtgatcaacaatgaagagatcttcgagagc 1270
QY 1244 agacgtccaaagcggtccaaactggtgcgaacacgcgccaaggaaggaagaagatccgag 1303
Db 1271 aaacgatgaagcggtctgataactgtgaggaagaagcgatgtgaagaagaaggtccggg 1330
QY 1304 aacagagacatgctgatagtcagatgatcggtgcgagcgaacacgcgagccgagctgcgc 1363
Db 1331 acgccgacgcgttccgtgcgagatgagcgtgcgc-----ttcgcgagcg 1375
QY 1364 cgatgcgagcggtgtcatcaccccggtgcacactgtctcacaaagggcatgtggcggtcg 1423
Db 1376 cggcgctgcagcggtccggtcgccggtgtgcacactgtgc---aggtcacagggcggtcg 1432
QY 1424 acgacccccagagcggtccacactgcgcaagagcaccagcaggtgtaggacatgtacc 1483
Db 1433 gacgcccccgagcgcccaatcacggtgtgcctcaccccggcacccggaagagacatgtacc 1492
QY 1484 cggttgtgtgtgcgacccggtgtcacagactaatcctaacgacagagaggtgcgcct 1543
Db 1493 cgggtgcggtgcggtgtgcgttcgcacagct---gctagaacgacccgcggaacagaggt 1549
QY 1544 cgtcgtcgccctcgaagcgacatcccaagtgcagatttttccctcagc 1593
Db 1550 ggatggcatcctcgtcggtcgacacatcgcgatctgtatttttccctcagc 1599

RESULT 12

AAV35025
ID AAV35025 standard; DNA; 2425 BP.
XX
AC AAV35025;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene homologue.
XX
KM Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, SchulzeJelefert PMJ;
XX
DR WPI; 1998-159149/14.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 6; 150pp; English.
XX
CC The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially in transgenic plants to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;

Query Match 35.8%; Score 573; DB 19; Length 2425;
Best Local Similarity 84.1%; Pred. No. 1.2e-112;
Matches 741; Conservative 0; Mismatches 5; Indels 135; Gaps 3;

QY 857 tccctcgtgatcctctctgtgtgtgtggaaccaagctgagatgatcatcatgagatg 916
Db 1529 ttcctcaacagatcctcttctgtgtgtggaaccaagctgagatgatcatcatgagatg 1588
QY 917 ccctggagatccaggaaccggcgagcgtcatcaagggggcccggtgtgcagccagca 976
Db 1589 ccctggagatccaggaaccggcgagcgtcatcaagggggcccggtgtgcagccagca 1648
QY 977 ac-aagttctctgtgtccacgcgccccgactggtcctcttcatacactgaactg 1035
Db 1649 acaagttctctgtgtccacgcgccccgactggtcctcttcatacactgaactg 1708
QY 1036 ttccagaacggttccagatggcgcatttgtgtgagagt----- 1076
Db 1709 ttccagaacggttccagatggcgcatttgtgtgagagtgtacgcaacgatgaact 1768
QY 1077 ----- 1076
Db 1769 tgtcagttaacatggtgttcaaggcaccgagtgccgctgatgaactgtcttgacggagat 1828
QY 1077 -----ggccaacgcccggcttgaagaatgtctaacacagcagatcggtgagc 1125

[illegible]

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RESULT 13
AAA52707
ID AAA52707 standard; cDNA; 678 BP.
XX
XX AC AAA52707;
XX
XX DT 27-OCT-2000 (first entry)
XX
XX DE wheat M10 homologue putative coding sequence #1.
XX
XX KW wheat; M10 homologue; disease resistance; ss.
XX
XX OS Triticum aestivum.
XX
XX FH Key Location/Qualifiers
XX FT CDS 3..664
XX FT /*tag= a
XX FT /product= "M10 homologue"
XX FT /partial
XX FT /transl_except= (pos:639..640,aa:Ser)
XX FT /note= "there is an apparent one nucleotide
FT deletion at this position, resulting in a frameshift"
XX
XX PN WO200036110-A2.
XX
XX PD 22-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-US30181.
XX
XX PR 18-DEC-1998; 98US-0112737.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX

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PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
DR WPI; 2000-431590/37.
P-PSDB; AAB01797.
XX
PT New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX
XX
PS Claim 2; Page 52; 79pp; English.
XX
CC The present sequence is a putative coding sequence for a Mlo homologue
CC from wheat. It was identified by searching a root and leaf cDNA library
CC for sequences encoding proteins similar to Mlo from *Hordeum vulgare*
CC (barley) and *Arabidopsis thaliana*. Mlo confers resistance to *Erysiphe*
CC *graminis* f. *sp. hordei* upon the plant, and its inactivation leads to the
CC priming of disease resistance even if the pathogen is not present. The
CC gene and protein can be used to create transgenic plants which have
CC increased disease resistance, as well as allowing researchers to find
CC other resistance-conferring genes and proteins.
XX
SQ Sequence 678 BP; 143 A; 206 C; 199 G; 130 T; 0 other;

Query Match	35.6%;	Score 569.8;	DB 21;	Length 678;
Best Local Similarity	92.0%;	Pred. No. 4.3e-112;		
Matches 612; Conservative	0;	Mismatches 52;	Indels 1;	Gaps 1;

[illegible]

Db 663 gatga 667

RESULT 14
AAA52704
ID AAA52704 standard; cDNA; 563 BP.
XX
AC AAA52704;
XX
DT 27-OCT-2000 (first entry)
XX
DE Soybean MLO homologue putative coding sequence #2.
XX
KW Soybean; MLO homologue; disease resistance; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 2..562
FT /*tag= a
FT /product= "MLO homologue"
FT /partial
FT /transl_except= (pos:452..455,aa:Xaa)
FT /transl_except= (pos:503..505,aa:Xaa)
FT /transl_except= (pos:530..532,aa:Xaa)
FT /transl_except= (pos:557..559,aa:Xaa)
FT /note= "Xaa=unknown"
XX
PN WO200036110-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US30181.
XX
PR 18-DEC-1998; 98US-0112737.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
XX WPI; 2000-431590/37.
DR P-PSDB; AAB01794.
XX
XX
PT New polynucleotide encoding a MLO homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX
PS Claim 2; Page 47; 79pp; English.
XX
CC The present sequence is a putative coding sequence for a MLO homologue
CC from the soybean. It was identified by searching a seed cDNA library
CC for sequences encoding proteins similar to MLO from Hordeum vulgare
CC (barley) and Arabidopsis thaliana. MLO confers resistance to Erysiphe
CC graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC priming of disease resistance even if the pathogen is not present. The
CC gene and protein can be used to create transgenic plants which have
CC increased disease resistance, as well as allowing researchers to find
CC other resistance-conferring genes and proteins.
XX
SQ Sequence 563 BP; 118 A; 171 C; 165 G; 105 T; 4 other;

Query Match 30.8%; Score 493.4; DB 21; Length 563;
Best Local Similarity 92.0%; Pred. No. 7.5e-96;
Matches 518; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 942 cgtcatcaaggggcccccgtgtgcgagccagcaacaagtctctgtgtccaccgcc 1001
DB 1 cgtcatcaagggggcccgtgtgtgagccagcaacaagtctctgtgtccaccgcc 60

QY 1002 cgactggtcctctctcatcacactgacgtgttccagaacggttccagatggcgca 1061
DB 61 cgactggtcctctctcatcacactgacgtgttccagaatgcgttccagatggcgca 120
PS

QY 1062 ttgtgtgacagtggtccacgcccggcttgaagaatgtaccacacgcatcggtc 1121
DB 121 ttctgtctggacagtggtccacgcccggcttgaagaatgtctccatatgtccatcggtct 180

QY 1122 gagcatcatgaagtggtgtgtgtgggttagctctccagttcctctgcagctatatgacct 1181
DB 181 gagcatcatgaagtggtgtgtgtgggttagctctccagttcctctgcagctatatgacct 240

QY 1182 cccctctacgctctgtctcacacagatgggatcaaacatgaagaggtccattctcgacga 1241
DB 241 cccctctacgctctgtctcacacagatgggatgaacatgaagaggtccattctcgacga 300

QY 1242 gcagacgtccaagcgctcaaccaactggcggaacacgccaaggaagaagaagtccg 1301
DB 301 gcagacgccaagcgctgacccaactggcggaacacgccaaggaagaagaagtccg 360

QY 1302 agacacgacatgtgtgtgtcagatgatcgcgacgcaacacgacgagcgtctgtc 1361
DB 361 agacacgacatgtgtgtgtcagatgatcgcgacgcaacacgacgagcgtctgtc 420

QY 1362 gccgatgccagcgccggtctcatcacccgtgcacctgtctcacaagggtatggcggtc 1421
DB 421 gccgatgccagcgccggtctctgtcacccgtgtgcantgtctcacaagggtatggcggtc 480

QY 1422 ggaacgacccccagagcggtgccacctgcgccaaaggaccagcaggtctaggtatgtta 1481
DB 481 ggaacgattcccaagagcggtccganctgcgccaaaggaccatgtgaggaagtangaatgtta 540

QY 1482 cccggtgtgtgtgtgcgacccgg 1504
DB 541 cccggtgtgtgtgtgcgacnccgg 563

RESULT 15
AAZ49564
ID AAZ49564 standard; cDNA; 1815 BP.
XX
AC AAZ49564;
XX
DT 07-APR-2000 (first entry)
XX
DE Maize MLO6 protein encoding cDNA.
XX
KW MLO6 protein; ZmMLO6; chromosome 5; mutation; recessive allele;
KW disease resistance; pathogen; anti-infective; antipathogenic; antiviral;
KW antifungal; antihelminthic; anti-arthropod; maize; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 46..1593
FT /*tag= a
FT /product= "MLO6 protein"
XX
PN WO200001722-A1.
XX
PD 13-JAN-2000.
XX
PF 07-JUL-1999; 99WO-US15255.
XX
PR 07-JUL-1998; 98US-0091875.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Briggs SP, Simmons CR;
XX
XX WPI; 2000-137196/12.
DR P-PSDB; AAY44605.
DR
XX
PT Creating or enhancing disease resistance in plants by modulating plant
PT resistance genes expression -
XX
PS Claim 1c; Page 70-71; 88pp; English.

